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GenCore version 5.1.6
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February 15, 2004, 05:50:07; Search time 18600 Seconds (without alignments) 11619.654 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Clonin	Syntheti	L38498 Cloning vec	26 His-3	327 His-3	129 His-3	15 Cloning	22 Shuttle	61 Shuttle	180 Cloning	AY222814 Cloning v	Murine ret	9 Sequence	AF402295 pk[BIG-al	10 Sequence	U04896 Cloning vec	86 Express	87 Express	AJ007659 Cloning v	2 Sequence	AF402779 Expressio	Sequence	0 Insulin-	11 Treat	O Treatmen	0 Interf	84 Clonin	ຸດ ຊ	7 Method	တ်	shuttle	9 Sequence	5 Sequenc	AX00886/ Sequence AX641960 Sequence			DNA linear SYN 02-SEP-1999		kan	stance.		14 dependent two-hybrid screens	
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	Db 2254 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGTAACGCAGGAGAACATGTGAG 2313 Qy 3071 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 3130 Db 2314 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA 2373	OY 3131 GGCTCCGCCCCCTGACGATCACAAAATCGACGCTCAAGTCAGGGGGGAACC 3190 	Oy 3191 CGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTGGTGCGCTCTCCTG 3250	Oy 3251 TICCGACCCTGCCGCTTACCGGAFACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCG 3310 2494 TICCGACCTGCCGCTTACCGGAFACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC 2553	QY 3311 TTTCTCATAGCTCAAGGTATCTCAGTTCGGTGTAAGGTCGTTCGGTCGAGCTGG 3370 Db 2554 TTTCTCATAGCTCAAGCTGTAAGGTATCTCAAGTTCGGTGTAAGGTCGTTCGCTCCAAGCTGG 2613	OY 3371 GCTGTGTGCACGAAACCCCCGTTCAGCCCGACGCTGCGCCTTATCCGGTAACTATCGTC 3430	OY 3431 THGAGTECAACCGGTAAGACACGACTTATCGCCACTGGCACGCCACTGGTAACAGGA 3490 2674 THGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCACCTGGTAACAGGA 2733	OY 3491 TTAGCAGAGCGAGGGTATGTAGAGAGGGTTCTTGAAGTGGTGGCCTAACTACG 3550 2734 TTAGCAGAGGAGGTATGTAGGGGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG 2793	QY 3551 GCTACACTAGAAQAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA 3610	OY 3611 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACGCTGGTAGCGGTGGTTTTTTG 3670 2854 AAAGAGTTGGTAGCTCTGATCCGGCAAACAAACCACGCTGGTAGCGGTGGTTTTTTG 2913	OY 3671 TITGCAAGCAGAGTTACGCGCAGAAAAAAGGATCTCAAGAAGTCCTTTGATCTTTT 3730 Db 2914 TITGCAAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTT 2973	Qy 3731 CTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT 3790 Db 2974 CTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGCT 3033	303	Dy 3195 3794 AGTGACCTCAGGGGAAAACGGGAAGACACTCATGAGATGCCTGCAAGCAA	OY 3795	Ay 3826 TCCTGCAGTTCGGGGCATGGATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCCACG 3885	Qy 3886 GATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCAGCTGAACCAA 3945
REFERENCE 2 (bases 1 to 6074) AUTHORS Bannasch, D. TITLE Direct Submission JOURNAL Submitted (30-0CT-1998) D. Bannasch, Institution Division of, Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKF2), Im	lberg, FRG	/ Day States	/codon_start=1 /product="hypothetical protein" /protein_id="CaB54527.1" /db_xref="G1:S830188"	~ X Z 4	<pre>misc_feature 434. 874 /note="Gal4 DNA binding domain" misc_feature 877. 905 /note="multiple cloning site"</pre>	CDS complement (31263506) /codon.start=1 /product="bleomycin resistance protein" /protein id="CAB54529.1"	/db_xref="G1:5830190" /translation="MTDQATPNLPSRDEDSTAAFYERLGFGIVFRDAGWILQRGDLM LEFFAHFGLDPLASWFSCCLRLDDLAEFYRQCKSVGIQETSSGYPRIHAPELQEWGGT MAALVDPDGTLAELIONELLAGIS	CDS complement (35274321) /codon start=1 /product="neomycin/kanamycin resistance protein" /protein id="CAB54528.1"	/db_xref="G1:5830189" /translation="MIROPGLHAGSPAAWVERLEGYDWAQOTIGCSDAAVFRLSAQGR FVLFVKTDLSGALNELQDBAARLSMLATTGVPCAAVLDVVTBAGRDWLLGEVPGQDL LSSHLAPARKVSIWADAWRRLHTLPPATCPFDYGAKHRIFRMAG1VDODDL	EHGGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY OUTALATRDIAEBLGGENADRFLVLVGIAAPDSQRIAFYRLLDEFF" Complement (4410. 4459) / dense "aninolycoside phosphotrangfarass"	promoter complement (4410, .4459) BASE COUNT 1593 a 1549 c 1380 g 1552 t ORIGIN	Query Match Best Local Similarity 94:5%; Pred. No. 0; Matches 2568; Conservative 0; Mismatches 5; Indels 145; Gaps 1;	QY 2711 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 2770	OY 2771 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG	CY 2831 CATTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 2890	GGCTT	2951

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Oy 5026 AGGGCTTCCCAACCTTACCAAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCC 5085 H 4414 AGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCTG	RESULT 2 AR260588 LOCUGUS LOCUGUS LOCUGUS DEFINITION Sequence 16 from patent US 6489542. ACCESSION AR260588 VERSION AR260588.1 GI:27311143 KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE AUTHORS Corbin.D.R. and Romano, C.P. AUTHORS Corbin.D.R. and Romano, C.P. TITLE JOURNAL FAATURES Location/Qualifiers SOURCE 1. 8489542-A 16 03-DEC-2002; FAATURES Location/Qualifiers SOURCE 1. 8489642-A 16 03-DEC-2002; FAATURES COUNT 1959 a 2355 c 2088 g 1947 t	Query Match
3274 GATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCAGCCTCAGGCAGCTGAACCAA 3333 3946 CTCGCGAGGGGATCGAGCCGCGGGGGGGGGGCGCGCGCGGGGGGGG	246 CAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCCA 634 CAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCCCA 306 CACAGTCGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGC 634 CAGGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 635 GCCATGGGTAAAACGGCCATTTTCCACCATGATATTCGGCAAGC 636 GGCCATGGGTCACGAAAAGCGCCCTTTCGTCCACTGAGCCTTGAGCCTGA 637 GCCATGGGTCACGAGAATCCTCGCCGTCGGGCCTTTAGGCCTGA 648 GTTCGGCTGGGCGCGAGCCCCTGATGCTCTTCGTCCAATCATCCTCAATCGACAAA 648 GTTCGGCTGGGCGCAGCCCCTGATGCTTCGTCCAAATCATCCTGATCGACAA 651 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	### ##################################

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3191 1963 3251 1903 3311 1783 3431 1723 3491 1663 3551	1543 AAAGAGTTGGTAGCTCTTGATCCGGCAAACCACCGCTGGTAGCGGTGGTTTTTTTT	3791 TATCGTCCAAAGCGCCCATCGTGCTCCCCCACTCCTGCAGTTCGGGGGCCATGGATGC 385 1363 TATCAAAAAGGTCTTCACCTAGATCCTTC	1327 GGGG 4031 AAAC 4031 GGGG 4031 GGGG 4031 GCAG 4031 GCAG 4151 GTCA 1147 GTCA 4211 GAGG
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RESULT 3 SYNBRANCG/ SYNBRANCG/ SYNBRANCG/ SYNBRANCG/ SYNTHETIC Plasmid pK18 (pBRNeo/pUC18) kanamycin resistance gene, Complete cds. ACCESSION WERSION WI726.1 G1:207845 COMPLETE Gloning vector ORGANISM Unidentified cloning vector ORGANISM ALTHORS Pridmore, R.D. TITLE JOURNAL MEDLINE PUBMED COMMENT COMENT COMMENT COMENT COMMENT COMMENT CO	PVLFVYTDLSGALMELQDEAARLSWIATTGVPCAAVLDVVTEAGENGILLGEVPGQDI ISSHLAPAEKVSIMADAWRRIHTIDPATCFPDQAKRRIERARTRAMEGLUGDELDE EHQGLAPAELFARLKARANGDEDLVVTHGDACLPNIAVERAGENDGLDE EHQGLAATRDIAEELGGEWADRFLVVYTHGDACLPNIAVERARENGGETUGGRIGGVADRY BASE COUNT 584 a 724 c 769 g 584 t ORIGIN Query Match Best Local Similarity 93.4%; Pred. No. 0; Matches 2403; Conservative 0; Mismatches 26; Indels 144; Gaps 1;	QY 2711 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCAACA 2770 Db 2443 CGTAATCATGGTCATACTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 2384 QY 2771 ACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGAGGTGCCTAATGAGTGAG	Qy 2891 ATTAATGAATGGGCCAAGGGGGGGGGTTTGCGTATTGGGCGCTTTCCGCTT 2950 Db 2263 ATTAATGGATGGCCGGGGGGGGGGGTTTGCGTATTGGGCGTTT 2204 Qy 2951 CCTCGGTCACTGACTGGCGGGGGGGGGTTTGCGTTTTGGGCGTTTCGGCTT 2204 Qy 2203 CCTCGGTCACTGACTGGCTCGGTCGGTTCGGCGGGGGGTATCAGCTCACT 2144 Qy 3011 CAAAGGCGGTAATACGGTTATCCACAGATCAGGGGGTATCAGCTCACT 2144 Qy 3011 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 3070 Db 2143 CAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG 2084 Qy 3071 CAAAAGGCCAGCAAAAAGGCCAGGAACCGTTAAAAAAGGCCGGTTTTTCCATA 3130 Db 2083 CAAAAGGCCAGCAAAAAACGGCAGAAAAAAAGGCCGGTTTGCTGGCGTTTTTCCATA 2190 Qy 3131 GGTTCCGCCCCCTGACGAACCGTAAAAAACGACGCTCCAAGTCAGAGGTTTTTCCATA 2190 Db 2023 GGCTCCGCCCCCTGACGAACCACAAAAATCGACGCTCCAAGTCAGAGGTGCCGAAAACC 1964

Kanamycin-resistance (KmR) gene fragment. ESSION 138498 1 GI:986977 EGB gene; cloning vector; kanamycin resistance. CaclB gene; cloning vector pKILI18 ORGANISM arificial sequences; vectors. AUTHORS Bernard, a sequences; vectors. AUTHORAL IN SETTING 18991 AUTHORAL Gene 1 to 2999 AUTHORAL Gene 1 to 2099 AUTHORAL Gene 1 to 2000 AUTHORAL Gene 1 to 2000 AUTHORAL Gene 2 to 2000 AUTHORAL Gene 1 to 2000 AUTHORAL Gene 2 to 3000 AUTHORAL GENE 3 to 3000 AUTHORAL	Db 2999 AGCRGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACACA
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                                                         or
cloning vector pXIII19
artificial sequences; vectors.

1 (bases 1 to 2999)
Bernard, P.
New card positive-selection cloning vectors with kanamycin chloramphenicol selectable markers
6000896
7557407
                                                                                                                                                                                                                                                                                                                                                                      Score 2218.4; DB 12; Length 2999;
Pred. No. 0;
0; Mismatches 26; Indels 144;
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                                                                                    lee_D.W., Haag_J.R. and Aramayo,R.
lee_D.W., Haag_J.R. and Aramayo,R.
lee_D.W., Haag_J.R. and Aramayo,R.
Submitted (03-DEC-2002) Biology, Texas A&I
College Station, TX 77843-3258, USA
Location/Qualifiers
1. 2604
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.larity 93.2%; Pred. No. 0;
Conservative 0; Mismatches
   Neurospora crassa
Curr. Genet. 43 (1), 17-23 (2003)
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Matches 2359; Conserv
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artificial integration vector pJHAM01
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1 (bases 1 to 2604)
Lee.D.W., HaagyJ.R. and Aramayo,R.
Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of
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                    /organism="his-3 integration vector pJHAM002"
/mol_type="genomic DNA"
/db_xref="taxon:220725"
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Matches 2359; Conservative 0; Mismatches
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Pred. No. 0;
0; Mismatches
/db_xref="taxon:220727"
/focus
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Matches 2359; Conservative
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Lee,D.W., Haag,J.R. and Aramayo,R.
Lee,D.W., Haag,J.R. and Aramayo,R.
Direct Submission
Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
College Station, TX 77843-3258, USA
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	4253 ATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCCACCCGGCCACAGTC 4312 1220 ATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCACCCCACCCGCCGCCACAGTC 1161 4313 GATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCCACAGTC 1372 1160 GATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCCATCGCCATG 4372 1100 GGTCACGACGACATCTTCCACCATGATATTCGGCAAGCAGCCATCGCCATG 1101 4333 GGTCACGACGACATCCTCGCCCTTCGGCCCTTTCGGCAACAGTTCGGC 4432 1100 GGTCACGACACACACACACCATCGATCCACCATCATCGCCAACAGTTCGGC 1101 4433 TGGCGCGAACCCTCGATGCTCTCGTCCAGATCCTCGATCGA

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| artificial sequences; vectors.
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| kirchner,0. and Tauch,A.
| Tools for genetic engineering in Corynebacterium glutamicum

Unpublished
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2 (bases 1 to 3210)
3 (kirchner,O. and Tauch,A.
Direct Submission
Submitted (15-JAN-2003) Department of Genetics, University of Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany Location/Qualifiers

pk19Meca2"

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Best Local Similarity 86.7%;
Matches 2434; Conservative 2769 2970 3009 3069 2889 2949 2829 2910 ઠે ద ઠે 쉱 circular SYN 23-MAR-2003 AY219859
Cloning vector pK19MECA2, complete sequence.
AY219859. G1:29164979

RESULT 10
AY219859/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

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Shuttle vector pEC-K19mob2
artificial sequences; vectors.

1 (bases 1 to 5695)
Kirchner, O. and Tauch, A.
Tools for genetic engineering in the amino acid-producing bacterium Unpublished
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"Organism="Shuttle vector pEC-K19mob2"
/mol type="genomic DNA"
/db_xref="taxon:224992"
/note="Bscherichia coli-Corynebacterium glutamicum shuttle
                                                                                                                                        CAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTC 5237
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                           CCCTTGTCCAGATAGCC 5177
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SDLETLVADLEELADELRARQRQEDAQ"
                                                      2 (bases 1 to 5695)
Kirchner,O. and Tauch,A.
Direct Submission
Submitted (22-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                         CGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
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codon start=1
trans1 table=11
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Shuttle vector pBC-K19mob2, complete sequence.
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|db_xref="G1:29242906"
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Db 3895 TGATAGCGTCCCCACCCGGCCACAGCGATCCAGAAAGCGGCCATTT 3836 Qy 4338 TCCACCATGATATTCGGCAAGCAGCCACCGATCGAGAAACCGAGCATTT 3836 Db 3835 TCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGAGAATCCTCGCCGTCG 4397 Qy 4398 GGCATGGCGTTGAGCATCGGCATCGGCTCAGAGATCCTCGCCGTCG 3776 Qy 4398 GGCATGCGCGCTTGAGCTTGGCGAACAGTTCGGCTGGAGCCCTGATGCTCTTCG 4457 Db 3775 GGCATGCGCGCTTGAGCTTGGCGAACAGTTCGGCTGGCGCAGACCCTTGTTTCG 3716 Qy 4458 TCCAGATCATCGAGCAAGACAGTTCGGCTGGCGCGAAGCTCCTTCG 3716 Qy 4458 TCCAGATCATCGAGCAAGACAGTTCCGAGTGCTCCTTCG 3716	Db 3715 TCCAGATCATCCTGATCGACTTCCGAGTTCCGAGTACGTGCTCCTCGATGCGA 3656 Qy 4518 TGTTTCGCTTGGTGGTCGAATGGGCAGTAGCGGATCAAGCGTATGCAGCCGCCGCATT 4577 Db 3655 TGTTTCGCTTGGTCGAATGGGCAGTAGCCGGATCAAGCGTATGCAGCCGCGCTT 3596 Qy 4578 GCATCAGCCATGATGGATACTTTCTCGGCAGGAGATGATGAGAGATGACGAGAATCCTGC 4637	3595 GCATCAGCCATGATACTTTCTCGGCAGGAGCAGAGTGAGT	3415 GCTGCGCAAGGAACGCCCGTCGTCGCCACGCCACGATAGCCGCGCTGCCTCGTCTTGGAGT 4758 TCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCCCCTGCGCTGAC 3415 TCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCCCCTGCGCTGAC	Qy 4818 AGCCGGAACACGGGGCATCACGACTGTCTGTCCCCAGTCATAGCCGAT 4877 B	Qy 4938 AACGATCCTGTCTCTTGATCAGATCTTGATCCCTGGGCCATCAGATCCTTGGC 4997 bb 3235 AACGATCCTCTTCATCTTGATCTTGATCCCCTGCGCCATCAGATCTTGGTGCTTGGC 3176 Qy 4998 GGCAAGAAGAATCTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCCA 5057 Db 3175 GGCAAGAAAAAAAGCCATCCAGATTTACTTTGCAGGGCTTCCCAACGTTACCAGAGGGGCCCCCA 3116	5058 GCTGGCAATTCGGGTCGCTTGCTGCTGTAAAACCGCCCAGTCTAGCTATCGCCATGTA 51 3115 GCTGGCAATTCCGGTTCGCTTGCTGTCATAAAACCGCCCAGTCTAGCTATCGCCATGTA 30 5118 AGCCCACTGCAAGCTACCTGTTCTTTGCGTTTTGCGTTTTCCCTTGTCAAAACCGCCAGTTTTGCCTATAGCTATAGCCTTTGTCAATAGCC 51	Db 3055 AGCCCACIGCAAGCTACCTGCTTTGCGGTTTCCCTTGTCCAAATAGCC 2996 Qy 5178 CAGTAGCTGACATTCATCGGGGTCAGCATTCTGCGGACTGGCTTTCTACGTGTTC 5237 [RESULT 12 AY219861/c LOCUS AY219861 DEFINITION Shittle vector pEC-K19MECA2, complete sequence. ACCESSION AY219861
AACAG AACAG AACTA AACTA AACTA AACTA AACTA AACTA AACTA AACTA	4795 AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACAACCGCTGGTTGTTTTTTTT	OY 3729 TTCTACGGGGTCTGATGGAAACGAAATCACGTTAGGGGATTTGGTCATGGG 3788 DD 4675 TTCTACGGGGTCTGACGTCAAACTCACGTTAAGGGATTTTGGTCATGGG 4616 OY 3789 ATTATGGTCG	Db 4555 TTTTTGGACGATATACAGGATTTTGCCAAAGGGTTCGTGTAGACTTTCCTTGGTGTATC 4496 Oy 3799ACCAAAGGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGG 3840 Db 4495 CAACGGCGTCAGCGGGACAGGATAGGTGAAGTAGGTGAGCCCACCCGCGAGCGGTTCCTTC 4436	3841 GCATGGATGCGCGGATAGCCGCTGCTGGATGCCGACGGATTTGCACCGGGGGTTTCCTGGATGCCGACGGATTTGCACCTGCCGGGGTTTCCTGGATGCCTGCC	4375 3948 4315 4008	Db 4255 GAAAAGGCGGCGGCATGAGCCTGTCGGCCTGCTGGCCGTCGGCCAGGGC 4196	Db 4135	OY 4218 CGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCC 4277

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                                                                                                                                      5869 GGCGTAATCATGGTCATAGCTGTTTTCCTGTGTGAATTGTTATCCGCTCACAATTCCACA
                                                                                                                                                                       CACATTAATTIGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCT
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                                                                                                                                                                                                                                                                                                           GCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGC
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                                       DB 12; Length 5869;
                                                                      141; Indels 231;
                                   Score 2088.4;
Pred. No. 0;
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                                     39.5%;
ilarity 86.7%;
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                                   Query Match
Best Local Similarity
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                              Shuttle vector pEC-K19MECA2
Shuttle vector pEC-K19MECA2
artificial sequences; vectors.

I (bases 1 to 5869)
Kirchner, O. and Tauch, A.
Tools for genetic engineering in the amino acid-producing bacterium Unpublished
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|organism="Shuttle vector pEC-K19MECA2"
|/ml_type="genomic DNA"
|db_xref="texon:224610"
|note="Escherichia coli-Corynebacterium glutamicum shuttle
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PVLFWKTDLSGALMELQDEARLSWHATTGWPCAYLDVVFEAGRDWLLLGEVPGQDL
SSHLAPAEKVSIMADAMRILHTLDPATCPFDHQAKHRIERAFTRWEAGLVDQDDLDE
ENGGLAPAELPARLFARMPDGEDLVVTHGBACLPNIWFENGRFSGF
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DASGDLIDOGRVUWINPERRADETARRHALIYOGYQLKAAGRELKDAKI IDAYEYAYNV
AQAVGADGREPDLPAMRDRITWARRYGYVAKGQPVVPARRVETGSRGRKALATWGR
RGAATSNARWADDESKYAOETRORLAEANKRREWTGELLELRVKTAILDARSGSVAD
PSTRELAGELGVSERRIQOVRKALGMEAKRGRPRAEN"
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db_xref="G1:29164985"
translation="MDLSDVALESDALDAAVDLKTVIGFFRALDTTDAPASRDWASAA
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IVLDIDVPSHQAGGKIEHVNPQVYAILEKWARLEKAPAWIGVNPLSGKCQLIWLIDPV
YAAAGKTSPNWRLLAATTEEWTRVFGADQAFSHRLSRWPLHVSDDPTAYKWHCQHDRV
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db_xref="G1:29164984"
translation="MTLADPQDTVTASAWKLSADLFDTHPEAMRCGSRGWTAEDRREL
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, Bielefeld D-33615, Germany
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gene="aph(3')-IIa"
note="aminoglycoside phosphotransferase"
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codon start=1
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gene="repA"
note="replication protein"
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Direct Submission
Submitted (15-JAN-2003) Department o
Bielefeld, Universitaetsstrasse 25,
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product="Aph(3')-IIa"
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/note="RP4-mob region'
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	TTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGG ATTATCGTCG ATTATCGTCG ATTATCGTCG ATTATCGTCG ATTATCGTCG ATTATCGCACGGATAACCCTCAGTGAACGATTTTTTTTTT	TCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGGAATCTCGTGATGGCAGGTT TCCGAAGCCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGGAATCTCGTGATGGCAGGTT TCCGAAGCCCCAACCTTTCATAGAAGCCGGCGGTGGAATCGGAATCTCGTGATGGCAGTT GGGCGTTGGTCGGTCGTTTTCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGA AGGCGATAGAAGGCGTTGCGCTTGCAATCGGAAGCGCTCAAAGCACCTCAAGA AGGCGATTGGTCGGTTGCGCTTCGAATCGGAGCGGCGTTAACCGTAAAGCACGCAAGGAAG CGGTCAGCCCATTCGCCGCCAACTGCGATCGGAGCGCGTTACCTTAAAGCACGCAAGGAAG CGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAACCGTAAAGCACGCAAGGAAG CGGTCAGCCCATTCGCCGCCAAGCCGACCCAAGCAGATATCACGGGTAACCGTAAAGCACCCAACGCTATTTCCGCCCAAGCCCAAGCCGAATTTCAGCAATATCACGGGTAACCGCAACGCTATTTTTTTT

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EHQGLAPAELFARLKAMPDGEDLVYTHGDACLPNIWVENGRFSGFIDGGRLGVADRY
QDIALATRDIAEELGGEWADRPLVLYGIAAPDSQRIAFYRLLDEFF"
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IVLDIDVPSHQAGGKIEHVNPQVYAILEKWARLEKAPAWIGVNPLSGKCQLIMLIDPV
YAAAGKTSPNWRLLAATTEEMTRVFGADQAFSHRLSRWPLHVSDDPTAYKWHCQHDRV
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DASGOLIOTOGYKVLWYRDERARDETAFRHALTVOYQUKAAGREKKOMKIITDAYENYNV
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RGAATSNARRWADPESKYAQETRQRLAEANKRREWTGELLELRVKTAILDARSOSVAD
                                                                                                                                                                                                                                                                                                                                                                                    translation="MTLADPQDTVTASAWKLSADLFDTHPEAMRCGSRGWTAEDRREI
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'product="positive effector of replication"
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protein id="AAL38582.1"
/db xref="GI:17386070"
PSTRELAGELGVSERRIQOVRKALGMEAKRGRPRAEN"
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Pred, No. 0;
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/gene≃"rep"
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/protein id="AA066594.1"
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Kirchner.O. and Tauch,A.
Direct Submitssion
Submitted (22-JAN-2003) Department of Genetics, University of Submitted (22-JAN-2003) Department of Genetics, University ef Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany Location/Qualifiers
                                                                                                                CAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCCAGG
                                                                                   CCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAA
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| Organism="Cloning vector pK18mob2" | Organism="Cloning vector pK18mob2" | Organism="Cloning vector pK18mob2" | Organism="Cloning vector pK18mob2" | Organism="Escherichia coli" | Organism="Escherichia col
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Kirchner,O. and Tauch,A.
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                                                               CACTGTCCCTTATTCGCACCTGGGGGTGCTCAACGGGAATCCTGCTCTGCGAGGCTGGCC 4158
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                                                                                                                                                            AAAGGCGGCCGGCCATGAGCCTGTCGGCCTACCTGCTGGCCGTCGGCCAGGGCTA
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                                                                                                                      -GAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCG
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2 (bases 1 to 3053)
Tauch, A., Kirchner, O., Loffler, B., Gotker, S., Puhler, A. and
Kalinowski, J.
Direct Submission
Submitted (12-JAN-2003) Department of Genetics, University of
Bielefeld, Universitatsstrasse 25, Bielefeld D-33615, Germany
Location/Qualifiers
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Pred. No. 0;
0; Mismatches 140;
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//note="RP4-mob region"
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Best Local Similarity 86.7%;
Matches 2423; Conservative
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cloning vector pK18PolyF2
artificial sequences; vectors.

1 (Dases 1 to 3053)
Tauch,A., Kirchner,O., Loffler,B., Gotker,S., Puhler,A. and
Kalinowski,J.
Efficient electrotransformation of Corynebacterium diphtheriae with
a mini-replicon derived from the Corynebacterium glutamicum plasmid
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                                                                      987 igerceaargescaegrasccesarcaascerarscascescececrificarcacears
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AY222811
AY222811.1 GI:29169334
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U	(7)	1570	σ	4886	24	AAD42469		Human aequorin-pBk
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ALIGNMENTS

WPI; 2002-217153/27

Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischaemia or myocardial ischaemia, autoimmune disorders and allergic conditions

Disclosure, Fig 31; 241pp; English

The invention relates to an isolated nucleic acid comprising pVGI.1 factor 2 (VGF-2) insert. The nucleic acid is useful rendothelial growth factor 2 (VGF-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell with the DNA and for treating a patient having chronic limb ischaemia or myocardial ischaemia, or a disorder selected from autoimmune disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. conditions), organ rejection, inflammatory conditions (e.g. disorders (e.g. Gaucher's disease), disease), diseases (e.g. cardiomyopathy), arthythmia, heart valve diseases, aneurymms, arterial occlusive disorders and embolism. This sequence represents the pVGI.1 expression vector containing the VEGF-2

Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 other;

540 540 900 900 120 120 GGGATTICCAAGICICCACCCCACIGACGICAAIGGGAGITIGTITGGCACCAAAAICA 180 180 240 ACGAGACITICCAAAATGICGIAACAACICCGCCCCAIIGACGCAAAIGGGCGGIAGGGC 240 306 241 AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTG 300 CATGCCGATTGGTGGGAGTAAGGTGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAG 360 careccearrecressagraaceresrarcarecresrarcarecresrecresrerrerrareasas 360 GCAACAGACGCGTCTAACACGGATTGGACGAACCACTGAATTCCGCATTGCAGATATT 420 GCAACAGACGGGTCTAACACGGATTGGACGAACCACTGAATTCCGCATTGCAGAGATATT 420 GACCATICACCACATIGGIGIG 480 GTATTTAAGTGCCCAGCTCGATACAATAAACGCCATTTGACCATTCACCACATTGGTGTG 480 9 CACCTGGGTTGGGATCCATCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCT caccressirioscarccarcarcacacrescressiricrecressister GAGTCCGGACTCGGACCTCTCGGACGCCGGACGCGGGTGAGGCCACGCCTTATGCA AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAAGCACGTG AAGCTTGACCTTATGCGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT TACCATCGTGATGCGGTTTTTGGCAGTACATCGATGGGCGTGGATAGCGGTTTGACTCACG 181 ACGAGACTITCCAAAATGTCGTAACAACTCCGCCCCATTGACGCCAAATGGGCGGTAGGGC **PCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT** Gaps 100.0%; Score 5283; DB 24; Length 5283; .larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; GTATTTAAGTGCCCAGCTCGATACAATAAACGCCATT 1 AAGCITGACCTTAIGCGACTT Best Local Similarity Matches 5283; Conser 541 601 301 361 421 481 61 121 121 181 241 301 361 421 481 Query Match 61

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ò	1381	TGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAAACTAGACAGA 144
Db	1381	IGIGICIOCAGAGCGGGGCTICGGCCIGCCAGGGGGGCCCCACAAGAACTAGACAGA 144
à	1441	AACTCATGCCAGTGTGTGTGTAAAAAAAAACTCTTCCCCAGCCAATGTGGGGCCAACGGA 150
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ά	1501	GAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACC 15
đ	1501	GAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCC 156
à	1561	CTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAA 1.
qq	1561	chaaalcerggaaahggechgtgaangnagaaagrecacagaaatgettgitaaaa 162
ò	1621	GGAAAGAAGTTCCACCAACCAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAG 1681
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Š £	1681	AAGGCTTGTGAG
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3901 TAGAACTCCGCGAGGTCCTCCAGCTCAGCAGCTGAACCCAACTCGCGAGGGATCG 3960 3961 AGCCCGGGGTGGCAACAACTCCAGCATGAGATCCCGGCGCTGGAGGATCATCCAGCCG 4020 4021 AGCCCGGGGTGGGCCCAACCTTCCGAGCTCCGGCGCTGGAGGATCATCCAGCCG 4020 4021 GCGTCCCGGAAACGATTCCGAACCTATCATAGAAGGCGGCGGTGGAATCCGAA 4080 4021 GCGTCCCGGAAACGATTCCGAACCTTTCATAGAAGGCGGCGGTGGAATCGAAA 4080 4081 TCTCGTGATGGCAGCTTGGTCGCTCGTTTTCGAACCCCAGAGTCCCGCT 4140 4081 TCTCGTGATGGCAGGTTGGCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTC 4140 4081 TCTCGTGATGGCAGGTTGGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTC 4140 4141 AGAAGAACTCGTCAAGAAGGCGATGGCTCGTTTTCGAACCCCAGAGTCCCGCTC 4140 4141 AGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTACCAGATCCCGGCATAC 4200 4201 CGTAAAGCACGAGAAGGCGATTGGCCCAAGCTTCGCGCAATCAGGAGCGGATAC 4200 4201 CGTAAAGCACGAGAAGCGATTGGCCCAAGCTCTCAGGAATATCACGGG 4260 4201 CGTAAAGCACGAGAAGAGCGCTTCGCCCCAAGCTCTCAGCAATATCACGGG 4260 4201 CGTAAAGCACGAGAAGAGCCCATTCGCCCCAAGCTCTTCAGCAATATCACGGG 4260	4261 TAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCAGCCGGCCACAGTCGATGAATC 4320 4261 TAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCACCC	10 GTGCTCGCTCGATGCATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCG	4681 TGACAGGCCAGCAGGCAGGCCGGCCGGCGGCCAGCCAGGCCAGGGGGG
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              CCTGCGCTGACACACGCGGCGCCATCACAGCCGCGTTGTTGTTGTTGTGCCCAG 7926
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                                                                                                                                                                                                                                                                                                               8227 Grccagaradcccagragcraacarrcarccagggrcagcaccgrrrcraggacraggr 8286
                                                                                                                                                                                                                                                                                                                                                    TICTAGGIGTICGCCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion construct pNAMK6.1. This is an enzyme hybrid which can be used for the liquefaction of starch. The enzyme hybrids contain amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Starch, liquefaction, sweetener, enzyme hybrid, endoglucanase, enzyme, cellulose binding domain, CBD, starch processing, alpha-amylase, saccharification, Termamyl-linker-CBD fusion, ss.
CCCTGCGCTGACAGCCGGAACACGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG
                                               CAGATCCTTGGCGGCAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA
                                                                                                                                                                8047 CAGATCCTTGGCGGCAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA
                                                                                                                                                                                         GAGGCCCCCCAGCTGCCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC
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                                                                   7927 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT
                                                                                            TCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uefaction of starch for, e.g. production of sweeteners -
prises use of enzyme hybrids including cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid NAMK.6 (termamyl-linker-CBDEGV) nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Pages 65-67; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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Humicola insolens.
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of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is selected from the Bacillus or cellulomonas endoglucanase, C. xylanase A or the Humicola insolens BdV sequence. The starch is liquefied by treating, in aqueous medium, with such an enzyme hybrid. A recombinant expression vector comprising a construct containing isolated DNA encoding enzyme hybrids with amylolytic activity, promoter and stop signals can be used to transform host cells for the production of the recombinant enzyme hybrids are useful in industrial starch processing affinity for the production of sweeteners. Hybrid enzymes have altered affinity for substrate and increased activity, resulting in at least 1 of reduced calcium ion dependence, reduced formation of Maillard reaction products and reduced effect of alpha-amylase on subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.2%; Score 2017.2; DB 19; Length 6136;
llarity 91.8%; Pred. No. 1.1e-303;
Conservative 0; Mismatches 53; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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3664 ITITITIGITIGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 3723

the origin of replication and replication start of promoter and coding sequence for tn9 kanamyci phrompter and coding sequence for tn9 kanamyci phosphotransferase. The plasmid was synthesis pacification describes a method for the synthemeter double-stranded polynucleotides. The generating a first set of oligonucleotides. The generating a first set of oligonucleotides. The method can be used for preparing polynuclinvolved in a biochemical pathway. In particul produce polynucleotides encoding enzymes, e.g. produces, polynucleotides encoding enzymes, e.g. prompter set, phosphofructokinaee-1, aldolase, beglyceraldehyde-3-phosphate dehydrogenase, phophosphogroglycerate mutuse, enclase or pyruvate also be used for the preparation of viral par and artificial genetic systems. 3847 ATGCGCGGATAGCCGCTGCTGGTTTCCTGGATG Query Match
33.9%; Score 1793.4;
Best Local Similarity 91.8%; Pred. No. 4.5
Matches 1980; Conservative 0; Mismatches 4800 CATAGGCTCCCCCCCCTGACGAGCATCACAA 4560 CIGGGCIGTGTGCACGAACCCCCCCCGTTCAGCC 4380 racectracacracaaaeaacacrarrreerar 4320 GGAAAAGAGTTGGTAGCTCTTGATCCGGCAA 4260 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAA 3787 AGATTATCGTCGACCAAAGCGGCCATCGTGCC 3127 CATAGGCTCCGCCCCCTGACGAGCATCACAA 3247 CCTGTTCCGACCCTGCCGCTTACCGGATACCT 4680 CCTGTTCCGACCCTGCCGCTTACCGGATACCT 3307 GCGCTTTCTCATAGCTCACGCTGTAGGTATCT 4620 GCGCTTTCTCATAGCTCACGCTGTAGGTATCT 3367 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCC 3427 CGTCTTGAGTCCAACCCGGTAAGACACGACTT 4500 cercircaerccaacceeraadacacerr 4440 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGC 3547 TACGGCTACACTAGAAGAACAGTATTTGGTAT 3607 GGAAAAGAGTTGGTAGCTCTTGATCCGGCAA TITGITIGCAAGCAGCAGATIACGCGCAGAAA 3727 TITICIACGGGICIGACGCICAGIGGAACGA Sequence 4800 BP; 1345 A; 1032 C; 1163 G; 3187 AACCCGACAGGACTATAAAGATACCAGGCGTT 4740 AACCCGACAGGACTATAAAGATACCAGGCGTT 3487 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGC 4200 ritriciacecercicacecrcacrecan 3667 ö g g g q ò g ò g ઠે g δ g à 셤 ઠ ò ä

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f the invention. The synthesis of replication	q	4141GCCCG 4137	
B. The method comprises es corresponding to the plus the minus strand and annealing. Ynucleotides encoding sequences	ර සි	3967 GGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCC 4026	
rticular, they can be used to . e.g. hexokinase, phosphohexose se, triose-phosphate isomerase, phosphoglycerate kinase,	<i>ò</i> €	7 CGGABAACGATTCCGAAGCCCAACCTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGT 4	
vate kinase. They can 1 particles, artificial genomes	<i>₹</i> 8	4087 GATGGCAGGTTGGGCGTCGCTTGGTCGTCTTTCGAACCCCAGAGTCCCGCTCAGAAGA 4146	
; 1260 T; 0 other; 4; DB 20; Length 4800; .9e-269;	8 %	4147 ACTOGTCAAGAAGGGGATAGAAGGGGATGGGCTGGGAATGGGGAGGGGGAAACGGTAAA 4206 	
Gaps GGCGA	දි සි	r 9	
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GCTCT	& 8	4327 AGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATGGCATGGGTCACGACGAGGT 4386	
GCGTG 46:	ò 4	4387 CCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGGGGAGCCCCT 4446	
CCAAG 45 ACTAT 34:	සි ර	4447 GATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTC 4506	
ACTAT 45 GTAAC 34 	රු සි	4507 GCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCA 4566 	
STAAC 44 CTAAC 35	è 8	4567 GCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGGAGGAGGAGGAGGATGACA 4626 	
4 E	8	4627 GGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAA 4686 	
SCTTC 43 STTTT 36	දි දි	4687 CGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCA	
37	දි දි	4747 CGTCCTGCAGTTCATTCAGGCACCGGACAGGTCGGTCTTGACAAAAAAAA	
TGATC 42 TCATG 37 	දි සි	4807 CCTGCGCTGACAGCGGAACACGGGGATCAGAGCGGCGATTGTCTGTTGTGCCCAGT 4866 	
AAAACTCAGGTTAAGGGATTTTGGTCAT- 4142 CTCCCCACTCCTGCAGTTCGGGGGCATGG 3846	& 43	4867 CATAGCCGAATAGCCTCTCCACCAAGCGGCCGGAGAACCTGCGTGCG	
TGCCGACGATTTGCACTGCCGGTAGAAC 3906	පි සි	7 CAATCATGCGAAA 	

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            4987 AGATCCTTGGCGCGAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAG 5046
                             3116 AGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGCTTCCCAACCTTACCAG 3057
                                                                        AGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT 5106
                                                                                                        3056 AGGGGGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACGGCCCAGTCTAGCT 2997
                                                                                                                                     5107 ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTG 5166
                                                                                                                                                                                                    TCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTT 5226
                                                                                                                                                                   2996 ArcaccardraAsacccacraccaaccraccracririciciriraccarraccarriraccarriraccarriraccarrac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for assembling gene or gene vector - comprises use of primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class IIS restriction endonuclease recognition site; endogenous mouse promoter element; itseue-specific gene expression; hormone-specific gene expression; ss; developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENSA 981, a monomeric DNA sequence produced by the invention
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                                                                                                                                                                                                                                                                                                                                                                              AAV33629 standard; DNA; 5594 BP
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isolating and identifying regulatory sequences from a cell, including those for enhanced biological activity, or tissue-specific, hormone-specific or developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3467 TGGCAGCCACTGGTAACAGGATTAGCAGAGGAGGAGGTATGTAGGGCGGTGCTACAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                        67; Gaps
                                                                                                                                                                                                                                                                                                  DB 19; Length 5594;
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                                                                                                                                                                                            Seguence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 other;
                                                                                                                                                                                                                                                                                       Query Match
31.3%; Score 1652.4; DB 19; Lengt
Best Local Similarity 85.4%; Pred. No. 3.2e-247;
Matches 1916; Conservative 0; Mismatches 261; Indels
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TACGTGTTCCGCTTCCTTTAGCAGCCCTTGC 5259
5080 CIGICCATAAAACGCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCT 5139
                 CGCCATGTAAGCCCACTGCAAGCTACCTGCT 3492
                                                               CAGATAGCCCAGTAGCTGACATTCATCCGGG 5199
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prising the PCV Rep gene.

ene, gene function, Geminivirus, CV; ss.

circle replication in host, comprises Rep gene, sequences open reading frame encoding

ucleotide that is capable of rolling ryotic host. The polymucleotide a virus, sequences that are cis on p protein can bring about RCR of the certain an bring about RCR of the me encoding a protein of interest to set, and optionally a multiple genera of family Geminivizidae, ynucleotide sequence is useful for nest neukaryotic cell, for nest neukaryotic cell, for hes texaryotic cell, for that gene, as gene sequence delivery that gene, as gene sequence delivery that gene, as gene sequence delivery that gene products to organisms nics. The present sequence represents mics. The present sequence represents nics. The present sequence corganisms and control of the own promoter, and instead by insertion of the bacterial

4325 GGGGGAACTCCCGCCCCACGGCTGCTGCCGATCTCGGTCATGCCGGGCCCGGAGGCGT 4266 3863 TGCTGGTTTCCTGGATGCCGATCGCCGATCATGCCGGTAAACTCCGCGAGGCGT 4266 4265 CCCGGAAGTTCGTGGACGACCTCCGACGTCGTCGTCCTCCAGGCCGCGCA 4206 3923 GCC	3983 CCAGCATGAGATCCCGGGGTGGAGGATCATCCAGCGGGTCCGGAAAACGATTCCGA 4042 4085 CGAGCCGGTCGACGTCGACGCTCCGGCGGTCGGCGTGAGCACCGGAA 4026 4043 AGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCTCGTGATGGCGGGGGGGG	4103 TCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCG	ATGCGTAAGGAGAAATACCGCATCAGGAAATTGTAAGCGTTAATAATTCAGAAGAACTC GTCAAGAAGGGATAGAGCGATCAGGAAATTGTAAGCGTTAATAATTCAGAAGAACTC	3785 GICAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGGGGGGATACCGTAAAGCAC 3726 4211 GAGGAAGCGGTCAGCCCATTCGCCGCCAACCCATTCAGCAATATCACGGGTAGCCAACGC 4270	TATGTCCTGATAGCGGTCCGCCACCCCAGCCGCCACAGTCGATGATCCAGAAAGCGGCCATTTTCCACATGATTCCAGAAAGCGGCCACAGTCCATGATTCCAGAAAGCGGCCATTTTCCACATGATTTCGGCAAGAGCAGCGCACAGGCATGAGTCATGAGTTTTCCACATGATTTTCGGCAAGCAGCACGCATGAGTCACGACGATGAGTCACCATGATTTCCACATGAGATCCTCGCCATGAGTCACGACGATCCTCGCCATTTTCCACATGATTCGGCAAGCGCATCGCCATGAGTCACGACGAGATCCTC	4391 GCCGTCGGGCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGGGGCCCCTGATG 4450	4511 GATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTACCGGATCAAGCGTATGCAGCCG 4570	4631 ATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 4690 3305 ATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTC 3246 4691 GAGCACAGCGCCAACAACGCCGTCGTGGCCACGACAATAGCCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT
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CC cloning vector. XX XX XX Sequence 5285 BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 other; Query Match Best Local Similarity 80.6%; Score 1634.4; DB 22; Length 5285; Best Local Similarity 80.6%; Pred. No. 1.9e-244; Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3; QY 2942 CTTCCGCTTCTCGCTCACTGACTCGCTCGGTCGTTCGGCTCGGGGGGGG	3062 ACATGTGAGGAAAAGGCCAGGAAAGGCCAGGAAACGGCAAAAAGGCCGCGTTGCTGGGGT 5165 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT 3122 TTTTCCATAGGCTCCGCCCCCTGAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTT 3122 TTTTCCATAGGCTCCGCCCCCTGAGGATCACAAAATCGACGTTGCTGAGGT 516 ACATGTGAGGTTCGCCCCCTGACGAACGCTAAAAATCGACGTTGCTGGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	3182 GGCGAAACCCGACAGGCTATAAAGATACCAGGCGTTTCGACACTCAGAGGGTGCGTGC	DD 4998 GCICICCIGITCCGACCCTGCCGCTTACCGGATACCTGTCCCCTTTCTCCCTTCGGGAA 4926 QY 3302 GCGTGGCGCTTTCTCATAGCTCACGCTGTCCGTTCGGTGAGGTCGTTCGCTT DD 4925 GCGTGGCGCTTTCTCATAGCTCACGTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT 4866 QY 3362 CCAAGCTGGGCTGTGCACGAACCCCCCGTTCAGCTGCGCTTATCCGGTA 3421	4 4 8 0 5 4 8 0 5 4 8 0 5 4 8 0 5 8 9 5 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	QY 3482 GTAACAGGATTAGCAGAGCAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC 3541 Db 4745 GTAACTAGGAGTATGTGTAGGCGGTGCTACAGAGTTCTTGAGTGGTGGC 4686 QY 3542 CTAACTACGGTACACTAGAACAGTATTGGTATTGGTATCTGCGCTCTGCTGAGCCAGTTA 3601 Db 4685 CTAACTACGGCTACACTAGAACAGTATTTGGTATCTGGCCTCTGCTGAGCCAGTTA 4685 CTAACTACGGCTAAACTAGAACAGTATTTGGTATCTGGCCTCTGCTGAAGCCAGTTA 4685		TGATCTTTTCTACGGGGTCTGACGCTCAGGAGGAAACTCACGTTAAGGGATTTTGG 	3795GIGGCGACGAGGCCACGAGGGCGAGGGCGAGGGCGGGCGG

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3681 GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC 3740
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                                       The invention provides a novel method for directing self-assembly of a gene having three or more fragments in a directionally and spatially ordered fashion to produce a gene vector. The method involves usage of primers, containing class IIS restriction endomuclease recognition sites, for isolation of these fragments. As described in the disclosure, the method may also use a vector for the incorporation and screening of endogenous mouse promoter elements for the incorporation and screening of endogenous mouse promoters. In the example given, plasmid VLSNO2, containing a circularily permuted mouse VL30 genome, was used in the construction of single long terminal repeat (LTR) vectors used in the method of the invention. In general, the method is claimed useful for isolating and identifying regulatory sequences from a cell, including those for enhanced biological activity, or tissue-specific, hormone-specific or developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1885 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACGCTACACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels 269; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.6%; Score 1618.2; DB 19; Length 6561; Best Local Similarity 86.7%; Pred. No. 6.1e-242; Matches 1911; Conservative 0; Mismatches 23; Indels 269; G
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6561 BP; 1629 A; 1593 C; 1696 G; 1643 T; 0 other;
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Example 3; Pages 110-113; 141pp; English.
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3245 GAGCACAGCTGCGCAAGGACGCCCGTCGTGGCCAGCCACGATAGCCGCCGCTGCCTCGTC 3186
                                            1185 TIGCAGTICATICAGGGCACCGGACAGGTCGGTCTTGACAAAAAAAAGAACGGGCGCCCCTG 3126
                                                                                                                                       4811 CGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCCAGTCATA 4870
                                                                                                                                                                                3125 CGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCGGATTGTCTGTTGTGCCCCAGTCATA 3066
                                                                                                                                                                                                                                  GCCGAATAGCCTCTCCACCCAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 4930
                                                                                                                                                                                                                                                                              3065 GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGACCTGCGTGCAATCCATCTTGTTCAAT 3006
                                                                                                                                                                                                                                                                                                                               CATGCGAAACGATCCTCATCCTGTCTCTTGATCTTGATCCTGGGCCCATCAGAT 4990
                                                                                                                                                                                                                                                                                                                                                                         CATGCGAAACGATCCTCATCCTGTCTTGATCAGAGCTTGATCCCCTGCGCCATCAGAT 2946
                                                                                                                                                                                                                                                                                                                                                                                                                        CCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGCCTTCCCAACCTTACCAGAGGG 5050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5051 GGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCG 5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class IIS restriction endonuclease recognition site; LTR; andogenous mouse promoter element; tissue-specific gene expression; hormone-specific gene expression; mouse VL30 genome; developmental-specific gene expression; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid VLSNO2 DNA sequence used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV33630 standard; DNA; 6561 BP.
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0y 4941 GATCCTCATCCTGATCTGATCTGATCCCTGCGCCATCAGATCCTTGGCGGC 5000 114 GATCCTCATCCTGTCTTTGATCTGATCCCTTGCGCTCAGATCCTTGGCGGC 655 9001 AAGAAAGCCATCCAGTTTACATTGCAGGCTTCCCAACCTTACCAGGGCGCCCCAGCT 5060 bb 654 AAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGGGCGCCCCAGCT 5050 904 GACAATTCCGGTTCGCTTGCTGCTCCATAAACCGCCCAGTCTACCAAGGGCCCCCAGCT 595 905 GACAATTCCGGTTCGCTTGCTGTTCATTACATTACTTACGCTTACCAATTCGCCATGTAAGC 5120 905 S121 CCACTGCAAGCTACCTGCTTCTTTGCGCTTGCCGTTTTCCCTTGTCCAATGTAAGC 535 906 GACAATTCCGGTTCGTTTCTTTTTGCGCTTGCCTTTTTTTCCTTTTTT	ABOUT 8 ABOT0294 XX ABOT0294 XX ABOT0294; XX ABOT0294; XX ABOT0294; XX ABOT0294; XX ABOT0294; XX ABOT0294; XX Nucleotide sequence of plasmid pVC0289. XX Pgy growth bornone seleasing hormone, GRRH; growth rate; RM feed fill chency, some octroph, growth related disorder; XM Bpy growth was: Insulin-like Growth Pertor-1; IGF-1; milk production; KM RM feed fill chency, some octroph, growth related disorder; XM Synthetic. Synthetic. Synthetic. BN WOZ00261037-A2. YE 12-DEC-2001; Z001WO-U848726. XX BAUG-2002. XX BAUG-2002. XX BAUG-2002. XX BAUG-2002. XX BAUG-2003. XX BAUG-2004. XX BAUG-2003. XX BAUG-2003. XX BAUG-2003. XX BAUG-2003. XX BAUG-2004. XX BAUG-2004. XX BAUG-2003. XX BAUG-2003.
1695	TCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGA 128 TCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGA 137 TAGCGGTCCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGA 137 TAGCGGTCCGCCACCACCCAGCCGCCAAGTCGATGAATCCAGAAAACCGGCCATTTTCC 434 TAGCGGTCCGCCAACCCAGCCAACACCAGCCATGAATCCAGAAAACCGGCCATTTTCC 436 ACATGATATTCGGCAAGCACCCAGCCAACACCCAGCACATCAACCCACCACCATTTTCC 436 ACATGATATTCGGCAAGCACCCAGCCATCGGTCACGACGAGATCCTCGCCGTCGGGC 125 ACATGATATTCGGCAAGACCGCATCGGCTAGGGTCACGACGAGATCCTCGCCGTCGGGC 125 ACATGATATTCGGCAAGACCGGCTTCCATCGGTCGGCGGCATTTTCC 446 ATGCGGCGCCTTGAACCGGCAACACCGGCTTCGGTCGGCGCGCATTTTCC 446 ATGCGGCCCTTGAACCGGCAACACCGGCTTCCGTCGGCGCCTCGATGCTCTTCGTCC 446 ATGCGGCCCTTGAACCGGCAACACCGGCTTCCATGGTCCGTCGATGCTCTTCGTCC 446 ATGCGCGCCTTGAACCGCAACACCGGCTTCCATGGTCATGCTCTTCGTCC 446 ATGCGCGCCTTGAACCGCAACACCGGCAACACGTCGAAGCCCCTGATGGTCTTCGTCC 446 ATGCGCGCCTTGAACCGCAACACCGGCAACACGTCGAAGCCCCTGATGGTCTTCGTCC 446 ATGCGCGCCTTGAACCGCAACACCCGACTTCCAGACGCCAACACCTCGATCGCTCCATTCGTCCC 447 AGATCATCGTTGATGATTTTTCTCGGCAGGTAACCTGAACCTCGATCGA

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cc of the female animal prior to or during gestation of the offspring under conditions where the nucleotide sequence is expressed. The coreasing suseful of improving or enhancing animal growth, for increasing growth hormone, lean body mass, IGP-I levels, feed efficiency, growth rate, ratio of somatorrophs to other commone-producing cells in a pituitary gland, and milk production in a confesping, and for delaying birth of an offspring, GRRH nuclear casis and vectors are used for diagnostic purposes in clinical endicine, both human and veterinary, eg. in treating growth-related disorders such as hypopituitary dwarfism resulting from abnormalities in growth hormone production, and in stimulating the growth and enhancing feed conversion efficiency of animals raised for meat, milk can egg production.

So Sequence 2192 BP, 486 A; 634 C; 601 G; 471 T; 0 other;
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-	and egg production.	i .
ญ	Sequence 2192 BP; 486 A; 634 C; 601 G; 471 T; 0 other;	සි <i>දි</i>
なわり	Query Match Best Local Similarity 82.8%; Pred. No. 1.2e-239; Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;	A 6
	2706 CIAGACGIAAICAIGGICAIAGCIGITIICCIGIGAGAAIIGITAICCGCICACAAIICC 2765	හී සි
	70 CTIGGCGIAATCAIGGICATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 129	3 8
	2766 ACACAACAIACGAGCCGGAAGCAIAAAGTGIAAAAGCCTGGGGTGCCTAATGAGTGAGCTA 2825	ਤੇ ਵੰ
	130 ACACAACATACGAGCCGGGAAGCATAAAGTGTAAAAGCCTGGGGTGCCTAATGAGTGCTAA 189	3 8
	2826 ACTCACATIAATTGCGTTGCGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGGCA 2885	3 E
	190 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 249	3 8
	2886 GCTGCATTAATGAATCGGCGAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 2945	ਤੇ ਨ
	250 GCTGCATTAATGAATCGGCCCAACGCGCGGGGAGAGGCCGCTTTGCGTATTGCGTCTTC 309	3 8
	2946 CGCTTCCTCGCTCACTGCTGCGCTCGGTCGCTCGCTGCGGGCGAGCGGTATCAGC 3005	à î
	310 GGCTTCCTCGCTCACTGGCTCGCTCGGTCGTTCGGCTGGGCGGGGGGGTCGTCG	<u> </u>
	3006 TCACTCAAAGGGGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAACAT 3065	S 6
	370 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 429	3 8
	3066 GTGAGCAAAAGGCCAAGCAAAAAGGCCAAGAAAAAGGCCGCGTTGCTGCGGTTTTT 3125	3 8
	430 GTGAGGAAAAGGCCAGCAAAAAGGCCAAGAAAAAAAAAA	<u> </u>
	3126 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG 3185	ž
	490 CCATRAGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGTCAGAGGTGGCG 549	3 8
	3186 AAACCCGACAGAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTGGTGCGCTC 3245	÷ €
	550 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCGCTC 609	3 8
	3246 ICCIGITCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305	à é
	610 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 669	5 6
	3306 GGGGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365	ð 6
	670 GGCGCTTTCTCATAGCTCACGCTGTAGCTATCTCAGTTCGGTGTAGGTCGTTCGCTCCCAA 729	3 8
	3366 GCTGGGCTGTGCACGCAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425	Š 6
	730 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCCCTTATCCGGTAACTA 789	3 8
	3426 TCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCGAGCG	j 5
	790 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAA 849	3 6
	3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545	Ì

d d	850	
à	3546	CTACGGCTACACTAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
අධ	910	TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT
ð í	o i	GGAAAAAGGGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT 366
g G	5	GTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTT 102:
පි සි	99	TTGAT 372
a G	03	.aagcagcagattacgcgcagaaaaaaggatctcaagaagatcctttgat 10
à	72	TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCAT 37
e e	1090	Ä
ò	3786	GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATG 3845
Dp	1108	1107
ò	3846	GATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905
QQ Qp	1108	1107
ò	3906	CTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGGATCGAGCCC 3965
qq	1108	1107
ζ	3966	GGGGTGGGCGAAGAACTCCCAGCATGAGATCCCCGGCGCTGGAGGATCATCCAGCCGGCGTC 4025
qq	1108	1107
à	4026	CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG 4085
d d	1108	1107
à	4086	TGATGGCAGGTTGGGCGTTGGTCGGTCATTTCGAACCCCCAGAGTCCCGCTCAGAAG 4145
q	1108	1117
ò	4146	AGAAGGCGATGCGCTGCGAATCGGGA
qq	1118	CTCGTCAAGAAGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATAAC
ð	4206	85-
qq	1178	CACGAGGAAGCAGTCAACCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGC
Š	4266	AACGCTATGTCCTGATAGCGGTCCGCACCCAGCCGGCCACCACTCGATGAATCCAGAA 4325
ପୁପ	1238	cectatetetetetetetetetetetetetetetetetet
ð i	N I	AGGGGCCATTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGA 43
Q C	σ.	AGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 135
ò	4386	GGGCATGCGCGCTTGAGCCTGGCGAACAGTTCGGCTGGCGC
qq	1358	circoccarcadearococcricasccrisacaracarroscriadecocaac
ò	4446	GATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTC
qa	1418	AIGCICITCAICAAACAICAICCIGAICGACAAGACCGGCITCCAICCGAGIACGI
È	4506	TGCGATGTTTCGCTTGGTGGT
qq	1478	detecandedaretricgericanecanteacaderacecantendecinate
Š	4566	AGCGGCGCATGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 1625

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Page 15

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3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
                                                                                  Example 2; Page 109-111; 113pp; English.
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                                                                                           1598 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 1657
                                                                                                                                                                                                      5046 GAGGGCCCCCAGCTGGCAATTCCGGTTGCTGTTGCTGTAAAAACCGCCCAGTCTAGC 5105
1538 AGCCGCCGCATTGCATCAGCCATGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 1597
                                                       4626 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACA 4685
                                                                                                                                                               4686 ACGICGAGCACAGCIGCGCAAAGGAACGCCGTGGTGGCCAGCCACGAIAGCCGCGCTGCC 4745
                                                                                                                                                                                                                                                                                ICGTCCTGCAGTTCATTCAGGGCACCGGACAGTCGTCTTGACAAAAGAACCGGGCGC 4805
                                                                                                                                                                                                                                                                                                                                                                                        CCCTGCGCTGACAGCCGGAACACGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 4865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4866 ICATAGCCGAATAGCCTCTCCAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGT 4925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1838 TCATAGCCGAATAGCCTCTCCCCAAGGGGCCGGAAACCTGCGTGCAATCCATCTTGT 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCCCAT 4985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1898 TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCTGCGCCAT 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGCCTTCCCAACCTTACCA 5045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1958 CAGATCCTTGGCGGCAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCA 2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2018 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 2077
                                                                                                                                                                                                                                                                                                                                 1778 cccriccorcadoccedaacacecececarcaeacacecearcarrererereres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass; Insulin-like Growth Pector-1; IGF-1; milk production; feed efficiency; somatotroph; growth-related disorder; hypopituitary dwarfism; meat production; egg production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Improving or enhancing growth, lean body mass, milk production, feed efficiency or Insulin-like Growth Factor-I levels, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kern DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2078 AACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of vector pSPc5-12-HV-GHRH.
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Comparing bequence represents vector parcellage.

The present sequence represents vector parcellage.

Confide encoding GHRH are used in the method of the invention. The apecification describes a method for improving or enhancing.

Confide encoding GHRH are used in the method of the invention. The apecification describes a method for improving or enhancing in an offspring.

Confide and for delaying birth of an offspring. The method comprises introducing a vector, encoding GHRH, into cells of the female animal prior to or during gestation of the offspring under conditions where prior to or during gestation of the offspring under conditions where the mucleotide sequence is expressed. The method is useful of sematoring or enhancing animal growth, for increasing growth hormone, lean body or enhancing animal growth, for increasing growth hormone, lean body mass, IGF-I levels, feed efficiency, growth rate, ratio of somatoring production in an offspring, and for delaying birth of an offspring.

Cother hormone-producing cells in a pituitary gland, and milk production in an offspring, and for delaying birth of an offspring.

CHRH muclei acids and vectors are used for diagnostic purposes in clinical medicine, both human and veterinary, e.g. in treating growth high and enhancing feed conversion efficiency of animals raised for meat, milk and egg production.
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                                                                                                                                                                                                                                                                                                     The present sequence represents vector pSPc5-12-HV-GHRH, which carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1412 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC
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                                                                                                                                                                                                      A method has been developed of treating urinary incontinence (UI) in mammals. The method comprises delivering a nucleic acid vector for the expression of a growth factor or neurotrophic factor in a tissue or tissues. The present sequence represents the actual lower sequence of plasmid piG052 nucleotides 1-3599 from the present invention. Due to the growth and stimulatory effects of growth factors and neurotrophic factors, introducing these factors to degenerated muscles in the neural improve UI by enhancing both their integrity and neural innervation.
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                                                                                                                                                                                                                                                                                                                                                                                         Score 1603.8; DB 19; Length 3599;
Pred. No. 1.1e-239;
0; Mismatches 27; Indels 392; Gaps
                                                                                                                  Treatment of urinary incontinence - by delivering nucleic acid vector for expression of growth factor or neurotrophic factor in
                                                                                                                                                                                                                                                                                                                                                             Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 other;
                                                                                                                                                                             Disclosure, Page 105-107; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         30.4%;
Dest Local Similarity 82.8%;
Matches 2022; Conservative
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Best Local Similarity
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04-FEB-1997;
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3 6 6 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
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                                                                    716 GCTGGGCTGTGTGCGCACGCCCGTTCAGCCCGACGCCGTGCCCCTTATCCGGTAACTA 775
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656 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 715

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1944 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 2003
                 5046 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2004 GAGGGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 2063
4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
                                                4506 CGCTCGATGCGATGTTCGCTTGGTGGTCGAATGGGCCAGGTAGCCGGATCAAGCGTATGC 4565
                                                                        1464 GGCTCGATGCGATGTTTCGCTTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 1523
                                                                                                 4566 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGGAAGGTGAGATGAC 4625
                                                                                                                         1524 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 1583
                                                                                                                                                 4626 AGGAGAICCIGCCCCGGCACIICGCCCAAIAGCAGCCAGICCCIITCCCGCIICAGIGACA 4685
                                                                                                                                                                        1584 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 1643
                                                                                                                                                                                                   4806 CCCTGCGCTGACAGCCGGAACACGGCGCCATCAGAGCCGATTGTCTGTTGTTGTGCCCAG 4865
                                                                                                                                                                                                                                                                                                                             1764 CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCCGATTGTCTGTTGTGCCCAG 1823
                                                                                                                                                                                                                                                                                                                                                      4866 TCATAGCCGAATAGCCTCTCCCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 4925
                                                                                                                                                                                                                                                                                                                                                                             1824 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 1883
                                                                                                                                                                                                                                                                                                                                                                                                         4926 TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCAT 4985
                                                                                                                                                                                                                                                                                                                                                                                                                                1884 TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCCAT 1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4986 CAGATCCTTGGCGGCAAGAAGCCATCCAGTTTACTTTGCAGGCCTTCCCAACCTTACCA 5045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGF-1; insulin-like growth factor I; skeletal alpha-actin gene promoter; muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS; Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2064 AACTGTTGGGAAGGCGATCGGTGCGGGCCTCTTCGCTATT 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actual sequence of IGF-1 containing plasmid pIG0552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV40796 standard; DNA; 3599 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0974572
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This sequence is the actual sequence for pIG0552 which is an example of a vector of the invention. The vector is for expression of a nucleic acid casequence in a cell, and comprises: (a) a nucleic acid caseatte containing a sequence encoding insulin-like growth factor-1 (IGF-1); (b) a sequence encoding region including one or more sequences necessary for expression of the nucleic acid caseatte, and lacking the coding a position for inserting the nucleic codid caseatte, and lacking the coding sequence of a gene with which it is naturally associated; and (d) a 3' flanking region, including a codid caseatte and comprises a sequence from a growth hormone 3'-UTR. The coefficient of the position for inserting the nucleic acid caseatte and comprises a sequence from a growth hormone 3'-UTR. The cherapy. It can be used for the delivery of IGF-I for treating diseases such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth disorders. They can be used for the delivery of IGF-I for treating diseases can be used for the disease such as Type I or Type II diabetes, genetic disease such as Type I or Type II diabetes, genetic disease such as Type I or Type II diabetes, genetic disease such as Charlanders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA
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                                                                                                                                                                                                                                                                                                                                                 New vector for expression of insulin-like growth factor-I containing a skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3' region from growth hormone 3'-UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 37-41; 115pp; English.
                                                                                                                                                          Coleman M, Demayo FJ, Schwartz R;
(BAYU ) BAYLOR COLLEGE MEDICINE. (GENE-) GENEMEDICINE INC.
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3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365
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                                                                3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
                                                                                                                                                                                                                                         3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGT 3305
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                                                                                                                  537 AAACCCGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTGGGGCGCTC 596
                                                                                                                                                                                                                                                                                                                        597 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGT 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A method has been developed of treating urinary incontinence (UI) in mammals. The method comprises delivering a nucleic acid vector for the expression of a growth factor or neurotrophic factor in a tissue or tissues. The present sequence represents the expected upper sequence of plasmid pigloss nucleotides 1.500 from the present invention. Due to the growth and stimulatory effects of growth factors and neurotrophic factors, introducing these factors to degenerated muscles in the urinary system can improve UI by enhancing both their integrity and neural innervation.
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Human; IGF-1; insulin-like growth factor 1; urinary incontinence; gene therapy; neurotrophic factor; ss.
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Best Local Similarity 82.8%; Pred. No. 1.9e-239;
Matches 2021; Conservative 0; Mismatches 28;
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This sequence is the expected sequence for pIG0552 which is an example of a vector of the invention. The vector is for expression of a nucleic acid as sequence in a cell, and comprises: (a) a nucleic acid cassette containing a sequence encoding insulin-like growth factor-I (IGF-I); (b) a cell, and comprises: (a) a nucleic acid cassette containing a sequence encoding insulin-like growth factor-I (IGF-I); (b) a containing containing region including one or more sequences necessary for skeletal alpha-actin gene; (c) a linker connecting the 5' flanking region of the nucleic acid cassette, and lacking the coding sequence of a gene with which it is neturally associated; and (d) a 3' flanking region, including a neturally associated; and (d) a 3' flanking region or both, where the call and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises a sequence from a growth hormone 3'-DTR. The cassette and comprises the calivory of IGP-I for Ireating diseases cuch as muscle arrophy, diabetes, genetic disease such as Type I or the passible and passes, a theroselectoric, cardiovascular, cerebrovascular, or peripheral vascular disease, haemophilia, inflammation and side-effects from anti-cancer and anti-viral druyes. The vectors can also be used to create transgenic animals for research or livestock improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
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Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC
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Best Local Similarity 82.8%; Pred. No. 1.9e-239;
Matches 2021; Conservative 0; Mismatches 28; Indels 392; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vector for expression of insulin-like growth factor-I - containing a skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3' region from growth hormone 3'-UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 37-41; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Coleman M, Demayo FJ, Schwartz R;
                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENEMEDICINE INC
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                                                                                                                                                                                                        01-DEC-1997;
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8 8	3006 TCACTCAAAGGGGTAATGGGTTATCCACAGAATCAGGGGATAACGGAGAACAT 3065 	qa	1095CGCTCAGAAG 1104
ે દ	31	à 8	4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCGCAATCGGGAGCGGCGATACCGTAA 4205
8 8	CCATAGGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	8 &	4206 AGAACGAGGAGAGGGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
3 8 8	CAIRAGCICCGCCCCCITANGAGGAICACAAAAAAAGGAGCICGAGGAGGIGGCG 53 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 32	ठे व	4266 AAGGCTATGTCCTGATAGCGGTCCGCCACACCCGGCCGCCACAGTCGATGAATCCAGAA 4325
3 & 5	3246 TCCTGTTCCGACCTGCGCTTACCGGATACCGGAAGCTCCTGGAAGCTCCTGGTGCGCTC 596 3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGT 3305 537 MCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 3305 537 MCTGTTCCGACCTCGCCTTTACCTGAAGCGT 550	ठे व	4326 AAGGGGCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGA 4385
8 8	GGCGCTTTCCCATAGCTCAAGGTATCCTCAGTTCGGGGTAGGTCCTTCGCTCCAA 33 [8 &	4386 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
8 8	GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 34	& g	4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAGGCCTTCCATCCGAGTACGTGCT 4505
8 8	TOSTCTTGACTCCAACCGGGTAACACACTTATCGCCACTGGCCACTGGTAA 34	ন ক	4506 OGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGC 4565
8 8	CAGGATTAGCAGAGGAAGTATGTAGGGGGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 35	8 &	4566 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625
g & 8	CTAGGGTACACAGGGAAGGAATTGTAGGCGGTGCTACAGAGTTCTTGAAGTGGGTGG	& A	4626 AGGAGATCCTGCCCCGGCCTTCGCCCAATAGCAGCCCAGTCCTTCCCGCTTCAGTGACA 4685
8 8 8	CGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACGCTGGTAGCGTGGTT 366	ò 8	4686 ACETCGAGCACAGCAGCAAGGAACGCCCGTCGTGGCCAGGCACGATGGTGGCCGCTGCC 4745
g & :	CGGAAAAGGGGTGGTTT 1 TTTTGTTTGCAAGGAAGGAGGGGGGGGGGGGGGGGGGGG	8 &	4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGC 4805
9 & :	TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAACTCTTTGAT 1 CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3 	& 48	4806 CCCTGCGCTGACAGCCGGAACACGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 4865
8 &	1077 CITTETACGAGGICTGA 1094 3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATG 3845	<i>8</i> 8	4866 TCATAGCCGAATAGCCTCTCCACCAAGCGGCCGGAGAACCTGCGGCATCCATC
g &	1095 1094 3846 GAIGCGGGAIAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905	ර් සි	926 1
g &	1095	8	S CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA S
q	1095 1094	ପ୍ର	S CAGATICCTTGGCGGCAAAGACCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 200
δλ	3966 GGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTC.4025	상 원	5046 GAGGGCCCCAGCTGCCATTCCGGTTCGCTGTCCATAAAACGCCCAGTCTTAGC 5105 2005 [11 1 1 1 1 1 1 1 1 1
면 당 전	1095 1094 4026 CCGGAAACGATTCCGAAGCCCTTTCATAGAAGGCGGCGGCGGAATCGAAATCTCG 4085	& 8	5106 TATCGCCATGTAAGCCCACTGCAAGCTACTTTCTCTT 5146 2065 AACTGTTGGAAAGGCGATCGGTGCGGCCTCTTCGCTATT 2105

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This invention describes novel expression vector systems containing RNA stability elements from 3. flanking sequences used for establishing expression of a nucleic acid sequence within a tissue. The vectors also facilitate enhanced expression in tissues and target expression with tissue specificity. The expression wectors can be used to treat diseases through gene therapy by targeting the vector to specific tissues. Diseases that can be treated include muscle arrophy associated with neurological, muscular or systemic disease, aging by causing tissues to express and secrete clotting factor into the circulation, atherogenesis and secrete clotting factor into the circulation, atherogenesis and secrete clotting factor into the circulation, atherogenesis and atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular disease by causing tissues to express factors involved in tissue metabolism. They can be used to replace genes of inherited genetic cells to produce particular proteins or RNA in vitro. To create transpend; animals which can be used for research into human diseases, casseshing novel therapeutic methods, assessing the effect of chemical and physical carcingens and for studying the effect of chemical and physical carcingens and for studying the effect of chemical and physical carcingens and for studying the effect of chemical and physical carcingens and for studying the effect of chemical and physical carcingens and for studying the effect of chemical and menuse response. These vectors provide controlled expression of the genes they carry and produce a significantly high level of expression.

Cubing 3 UTR sequences reduces the decay rates of the mRNAs encoded by the vectors which teachers and expression.
                                                                                                                                                                                                                     Plasmid pIG0335; expression vector; treatment; disease; RNA stability element; game therapy; muscle atrophy; neurological; muscular disease; systemic disease; ading; trophic factor; haemophilia; clotting factor; atherogenesis; atheroscierotic; cardiovascular; cerebirovascular; peripheral-vascular disease; hormone deficiency; diabetes; transgenic animal; carcinogen; regulatory element; limine response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5707 BP; 1221 A; 1634 C; 1576 G; 1276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New expression vector system useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DeMayo FJ, O'Malley BW, Schwartz RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 17-17F; 67pp; English.
                                         AAX88055 standard; DNA; 5707 BP
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94US-0209846.
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                                                                                                                                08-SEP-1999 (first entry)
                                                                                                                                                                            Plasmid pIG0335 DNA.
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09-MAR-1994;
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Query Match 30.3%; Score 1602.2; DB 20; Length 5707; Best Local Similarity 82.8%; Pred. No. 1.9e-239; Matches 2021; Conservative 0; Mismatches 28; Indels 392; Gaps

ДD		Qy 4926 TCAATCATGCGAAACGATCCTCATC
දු දු	3846 GATGCGCGGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905	5342
à	CTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCC	
qu	4552 4551	5402
È	3966 GGGGTGGGCGAAGAACTCCCAGCATGAGATCCCCCGCGCTGGAGGATCATCCAGCCGGCGTC 4025	5462 GAGGGCCCCCAGCTGGCAATTCCCC
ΩÞ	4552 4551	5106
λò	4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG 4085	5522
Ω	4552	
ζζ	4086 TGATGGCAGGTTGGTCGCTTGGTCGTCATTTCGAACCCCAGAGTCCCGCTCAGAAG 4145	RESULT 15 AAZ40417
Ω	4552	ID AAZ40417 standard; DNA; 5966 BP.
Sy Db	4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 4205 	AC AA240417; XX X 15-FEB-2000 (first entry)
à	4206 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCC 4265	XX DE Plasmid pIN0961 containing mouse II
QQ	4622 AGCACGAGGAAGCGGTCGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4681	KW Wild type, human; interferon-alpha KW promoter; growth hormone; untransl.
<u>ک</u> ۾	4266 BACGCTATGTCCTGATAGGGGTCGGCACACCCAGGCGGCCACAGTGGATGAATCCAGAA 4325	cancer; ir
λŏ	AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCCATGGGTCACGAGA	
. Q Q	4742 AAGGGGCCATTTTCCACCATGATATTCGGCAAGCAAGGCATCGCCATGGGTCACGAGA 4801	XX PD 23-SEP-1999.
à	TCCTCGCCGTCGGGCATGCGCGCTTGAGCCTCGCGAACAGTTCGGCTGGCGCGAACCCC	12-MAR-1999; 99WO-US0539
ą a	TCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC	19-MAR-1998; 980S-0
රු සි	4446 IGATGCICTICGICCAGAICAICCIGAICGACAAGACGGGCIICCAICCGAGIACGGCT 4505	PA (GENE-) GENEMBDICINE INC. XX DI Nordetrom I Dericle P. Rolland
3 &	CGCTCGATGCGATGTTTCGCTTGGTGGATGGGGCAGGTAGCCGGATCAAGCGTATGC	WPI; 1999-562116/47.
අධ	4922 CGCTCGATGCGATGTTTCGCTTGGTCGAATGGGCAGGAGAGCGGATCAAGCGTATGC 4981	XX PT New plasmids containing an interfer
જે દ	4566 AGCCGCCGCATTGCATCGAGCCATGATGGATACTTTCTCGGCAGGAGGAAGGTGAGATGAC 4625	creatment
ב מ	AdeleGeneder i Igenzinergene zur 1941 der inzenteren der der er der der der der der der der	
SP 42	AGGAGATICTIGCOCCCGGGCACTICGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	CC (CMV) promoter transcriptionally if
λō 1	ACTICAGACACACTGCCCAAGAAACGCCCGTCGTGGCCAGCACAATAGCCGCGCTGCC 47	
a 8	ACGICGAGCACCICCACAGCACCCCGICCTGGCCAGCCACCCATAGCCGCGCGCGCCGCGC	AA Sequence 5966 BP; 1421 A; 1627 C;
s a	14.48 TOTTCCTCCAGTTCATTCAGGCACCGGACGGGCTTGAGAAAAAAAA	Query Match 30.3%; Score Best Local Similarity 83.5%; Pred. Matches 2005. Conservative 0.7 MJ.
ž d	4806 CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 4865	ATCATGGTC
λ	TCATAGCCGAATAGCCTCTCCAAGCGGCCGGAAACCTGGGTAATCCATCTTGT	DD 60 CITGGGGTAATCAIGGTCAIAGCIG Qy 2766 ACACAACAIRCGAGCGGAAGCAIA
q	5282 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT 5341	

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re 1600; DB 20; Length 5966;
1. No. 4e-239;
dismatches 5; Indels 392; Gaps 1;
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                                                                            ATCAGITTACTITGCAGGGCTICCCAACCITACCA 5045
                                                                                                                                                       GGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105
CCTGTCTCTTGATCAGATCTTGATCCCTGCGCCAT 4985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid comprising a cytomegalovirus linked with an interferon alpha a growth hormone 3'-untranslated resents the plasmid plN0961 which 2 [IL-12) gene. The plasmids can be ndition or disease, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feron-alpha coding sequence, used for
lition or disease, particularly cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                na; plasmid; cytomegalovirus; CMV; slated region; UTR; mammal; disease;
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                                                                                                                                                                                                                                     GCTACCTGCTTTCTCTT 5146
                                                                                                                                                                                                                                                                          cegecciericeciair 5562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-12 sequence.
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QY 3906 CTCCGCGAGGTCGTCCAGCCTCAGGCAGCTGAACCAACTCGCGAGGGATCGAGCCC Db 1098	QY 4086 TGATGGCAGGTTGGGCGCTCGTTTCGAACCCCAGAGTCCCGCTCAGAAG Db 1098	Qy 4266 AACGCTATGTCCTGATAGCGGTCCCCACCCGGCCACGTCGATGAATCCAGAA Db 1228 AACGCTATGTCCTGATAGCGGTCCGCCACCCCAGCCGGCCACAGTCGATGAATCCAGAA Qy 4326 AAGCGGCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCAGAGAAA Db 1288 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGAGAAAAATTTCGGCAAGCAGAGAACAGTTTTCGCAAGAAAAATTTCGGCAAGCAGAGAAAAATTTTCGGCAAGAAAAATTTTCGGCAAGAAAAAATTTTCGGCAAGAAAAATTTTCGGCAAGAAAAAATTTTCGGCAAGAAAAAAAA	09 4446 TGATGCTCTTCGTTCGATCATCCTGATCGACGGCTTCCATCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	Qy 4626 AGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACA Db 1588 AGGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCTTCCCGCTTCAGTGACA Qy 4686 ACGTCGAGCACGCAGCAACGAACGCCGTCGTCGCCAACGACAACGACACGACGACGACGATGCCGCTTCCCGCTTCGCTGGCCGATGGTCGCTGGTCGATGGCCGATGGTCGTTGGCCGATGGTCGTTGGCCGATGGTCGTGGCCGATGATAGCCGCGCTGCCTGC	03
120 ACACAACATAATTGGGTGGGAAGCGTTAAAGCCTGGGGTGCCTAATGAGTGAG	TCACTCAAAGGCGGTAATACGGTTATCCAGAGTGGTTCGGTTCGGGGGGGG		GCTGGGCTGTGTGCAGAACCCCGTTCAGCCGCTGCGCTG	840 CAGGAITAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 899 3546 CTACGGCTACACTACAAGAACAGTATTGGTATCTGCGGCTCTGCTGAAGCCAGTTACCTT 3605 900 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 959 3606 CGGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAACCACGTGGTAGCTTT 3665 960 CGGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAAAAAA	TITIGITIGANGCAGAGAGATTACGGGGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 372 TITIGITIGCAAGCAGATTACGGCGGAAAAAAAGGATCTCAAGAAGATCCTTTGAT 107 TITIGITIGCAAGCAGATTACGCGCAGAAAAAAAGATCTCAAGAAGATCCTTTGAT 107 CITITCTACGGGGGTCTGACGTCGGAACGAAACTCACGTTAAGGGATTTTGGTCAT 378 CITITCTACGGGGGTCTGA

Oy 4986 CAGATCCTTGGCGGCAAGAAAGCCATTTACTTTGCAGGCTTCCCAACCTTACCA 5045

Db 1948 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGTTCCCAACCTTACCA 2007

Oy 5046 GAGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCCATAAAACCGCCCAGTCTAGC 5105

Db 2068 AA 2069

Search completed: February 15, 2004, 11:11:36

Job time: 1314 8ecs

7, Appli 147, Appl 4, Appli 14, Appli 33, Appl 4, Appli 50, Appli 6, Appli

Sequence Sequence Sequence Sequence Sequence

US-09-380-190A-14 US-09-026-343-33 US-09-044-856A-7 US-09-044-855A-7 US-09-024-855A-7 US-09-024-855A-7 US-09-026-408-14 US-09-026-408-14 US-09-027-287-50 US-09-027-287-50 US-09-024-796A-10 US-09-024-796A-10 US-09-044-796A-10 US-09-044-796A-10

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGCCA
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; Sequence 16. Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.;
; APPLICANT: Romano, Charles P.;
TITLE OF INVENTION: Improved Method for Transforming Plants to Expr.;
TITLE OF INVENTION: delta-Endoctoxins
; TITLE OF INVENTION: delta-Endoctoxins
; FILE REFERENCE: 38-21 (13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NOS: 18
; SEQ ID NO : 16
; SEQ ID NO : 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: gene
LOCATION: (3666)..(5573)
OTHER INFORMATION: completely synthesized
US-09-186-002-16
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Best Local Similarity 93.4%;
Matches 2409; Conservative (
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ORGANISM: Artificial Sequence
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                                                                                                                                            February 15, 2004, 01:53:42 ; Search time 272 Seconds (without alignments) 8572.894 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                     5283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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                         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-05-554-929-1/C
; Sequence 1, Application US/09554929
; Patent No. 6521427
; GENERAL INFORMATION:
; APPLICANT: Evans, Glan A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes;
; FILE REPRESENCE: P-EA 4749
; CURRENT APPLICAND NUMBER: US/09/554,929
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 4800;
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; OTHER INFORMATION: Synthetic plasmid US-09-554-929-1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                  <u> AGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT</u>
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US-02-380-190A-29/C
US-02-380-190A-29/C
j Sequence 29, Application US/09380190A
j Patent No. 6410220
j GENERAL INFORMATION:
j GENERAL INFORMATION:
j TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
j TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT,
STREET: 119 NORTH FOURTH STREET, SUITE
CITY: MINNEAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03918
PILING DATE: 28-FBE-98
ATTORNEY/AGENT INFORMATION:
NAME: MUBTING, ANN M.
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APPLICATION NUMBER: US/09/380,190A
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-380-190A-29
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CLASSIFICATION: <Unknown>
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TELEFAX: 612-305-1228
N FOR SEQ ID NO: 29:
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
LENGTH: 5594 base pa
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1314 ACCATOLATATICAGGAACTGGGGAACTGGGGGGGGGGGGGGGGGGG	RESULT 8 US-08-472-809B-8 Sequence 8, Application US/08472809B Sequence 8, Application US/08472809B Sequence 8, Application US/08472809B Sequence 8, Applicant Schwartz, Robert J. APPLICANT: DeMayo, Franco J. APPLICANT: O'Malley, Bert W. IIILE OF INVENTION: Expression Vector Systems and
GCGGCTTACCGGATACCTGTCGCCCTTTCTCCCTTCGGGAAGCGTGGGGCTTTCTCTAATG GCCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGGCTTTCTCTAATG CTCACGCTGTACCTCGGCTTTCTCTCCTTCGGGAAGCGTGGGCTTTCTCAATG CTCACGCTGTACTTCGGCTTTCTCTCCTTCCTCCAAGCTGGGCTTTGAGTCCAA CCAACCCCCCGTTCAGCCCGTTCGGCTTACCGTTCAAGTCTTCAATGCTCCAA CCAACCCCCCGTTCAGCCCGTTCGGCTTACCGGTAACTATCGTCTTCAAGTCCAA CCAACCCCCCGTTCAGCCCGTTCGGCAGCACCAACTACCGTTCAAGTCCAA CCAACCCCCCGTTCAGCCCGTTCGGCAGCACCAACTACCGTTCAAGTCCAA CCAACCCCCCGTTCAGCCCGTTCGGCAGCACCAACTACCGTTCAAGTCCAA CCAACCCCCGTTCAGCCCGTTCCGCAGCACCAACTACCGTTCAAGTTCAA CCAACCCCCGTTCAACCAACAACAACAACAACAACAACAACAACAACAAC	4221 TCAGCCCATTCGCGCCCAAGTTTTCAGCAATATCACGGGTAGCCAAGGCTATGTCCTGA 4280

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                                                                                                                                                                                                       TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGT
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                                                           3934 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG
                                                                                              3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCTCCTTC
                                                                                                                                     3994 AAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTC
                                                                                                                                                                        TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                   COMPUTER: DESCRIBED COMPUTER: DESCRIBED COMPUTER: DESCRIBED COPERATING SYSTEM: IBM P.C. DOS 5.0 SCTURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B FILING DATE: June 7, 1995
CLASSIFICATION DATA: APPLICATION NUMBER: 08/209,846
FILING DATE: MARCH 9, 1994
APPLICATION NUMBER: 08/209,846
FILING DATE: MARCH 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: NO. 5925564ember 6, 1991
ATTORNEY AGENT INFORMATION:
TITLE OF INVENTION: Method of Use
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 801te 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: SIS" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAWE: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERAX: (213) 955-0440
INFORMATION POR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
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Best Local Similarity 82.8%;
Matches 2021; Conservative (
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STRANDEDNESS: double
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MOLECULE TYPE: CDNA
US-08-472-809B-8
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APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGER
TITLE OF INVENTION: THE HPV INVENTION: 119
                                                                                                                                                                                     COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
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STRANDEDNESS: sing
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                          4622 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4681
                                                                              AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGACGAATCCAGAA 4325
                                                                                                                                                              4326 AAGCGGCCATTITCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCACGACGAGA 4385
                                                                                                                                                                                                                                               TCCTCGCCGTCGGCCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
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                                                                                                                      4682 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAA 4741
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Sequence 7, Application US/08948378A, Patent No. 6013258, GENERAL INFORMATION:
APPLICANT: Chicz, Roman M. APPLICANT: Chicz, Roman M. APPLICANT: Collins, Edward J.
US-08-948-378A-7/c
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3008 ACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 3067
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COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,378A

FILING DATE: 09-0CT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 34,819

REGISTATION NUMBER: 34,819

REGISTATION NUMBER: 08191/004001

TELEFAX: 617-543-8906

TELEFAX: 617-543-8906

TELEFAX: 617-543-8906

TELEFAX: 200154

INFORMATION FOR SQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 4665 Dase pairs
IMMUNOGENIC PEPTIDES FROM
THE HPV B7 PROTEIN
19
                                                                                                                        Richardson, P.C.
                                                                                                        STREET: 225 Franklin Street CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                     Length 4665;
                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                 Score 1571.6; DB 3;
Pred. No. 0;
0; Mismatches 114;
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NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERNCET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-169-425C-7
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.3%;
Matches 1850; Conservative
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                                                          704 Grerideadricarreaddeacacedacadgredererreacaaaaadaacedgeeeee 645
584 ATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGACCTGCGTGCAATCCATCTTGTTC 525
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86.3%; Pred. No. 0;
tive 0; Mismatches 114; Indels 180; Gaps
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Chicz, Roman M.
APPLICANT: Hedley, Mary Lynn
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: INMUNOSENIC PEPTIDES FROM THE HPV B7
TITLE OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSERE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                    524 AATCATGGGAAACGATCCTCATCCTGTCTTTG 481
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
FILING DATE:
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PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT:
NAME: Fraeer, Janis K.
REGISTRATION NUMBER: 34,819
REPERENCE/DOCKET NUMBER: 08191/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09759960
Patent No. 6582704
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
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Matches 1850; Conservative
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IDNESS: double
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STRANDEDNESS:
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US-09-759-960-7/c
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2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC 2505 2445 3188 ACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 3247 2385 3307 2384 chérrodakocordececria code a racción de controlece con controlece de controlece d 3487 2085 3667 3727 3068 GAGCAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTTTCC 3127 3187 3367 2264 rédécrérérécakédakécécécérréakécédakédécrédécétrarécédrakérakétak 2205 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 2145 3488 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT 3547 2025 1905 3819 3900 3961 3368 TGGGCTGTGTGCACGAACCCCCCGGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 3427 3548 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG 3607 1965 TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA 1845 1784 TCTAAAGTATATATGAGTAACCTGAGGCTATGGCAGGGCCTGCCGCCCCGGACGTTGGCTG 1725 ------TAGAACTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAAC 3946 1664 CGTATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGAA 1605 1604 CCCCGCGTTTATGAACAAACGACCCAAACACCGTGCGTTTTTATTCTGTCTTTTATTATTGCCG 1545 796E 990009-----2504 ATAGGCTCCGCCCCCTGACGACCATCACAAAAATCGACGCTCAAGTCAGAGGGGGGGCGAA CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGTGG 3308 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 2144 GGATTAGCAGAGCGAGCTATGTAGGCGGGGCGTACAGAGTTCTTGAAGTGGTGGCCTAACT 2084 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG 3608 GAAAAAGAGTIGGIAGCICTIGAICCGGCAAACAAACAACCACCGCIGGIAGCGGIGGIITITI TIGITIGCAAGCAGCAGATIACGCGCAGAAAAAAAGGAICTCAAGAAGAICCTTIGAICT 1964 Trigriridchadchadchadrincecachahahahahadarcrichadhadarcrirightor TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGA 3841 GCATGGATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGG 2444 ACCCGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTGGTGGGCTCTC 3428 GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCAGCCACTGGTAACA 2024 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACAACCGCTGGTAGCGGTGGTTTTT -----CCCCACTCCTGCAGTTCGGGG

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2075 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGGCTCTC 2134
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                           APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL. TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF
                                                                                                                                                               CORRESPONDENCE ADDRESS:

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
GITY: MINNEAPLIS
CITY: MINNEAPLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
COMPUTER: ISM FC COMPATIBLE
COMPUTER: ISM FC COMPATIBLE
COMPUTER: DATE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/380,190A
FILING DATE: 26-Aug-1999
CLASSIFICATION NATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28 = PEB-98
ATTORNET/AGENT INFORMATION:
NAME: MUBTING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
INFORMATION POR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-380-190A-26
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STRANDEDNESS: single
                                                                                                                                               NUMBER OF SEQUENCES:
GENERAL INFORMATION:
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                                                                                                                                           GGAAAACGATTCCGAAGCCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTG' 4087
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RESULT 9 US-09-380-190A-26 ; Sequence 26, Application US/09380190A ; Patent No. 6410220

2255 TGGGCTGTGTGCACGCACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 2314

3368 TGGGCTGTGTGCACGAACCCCCCGGTTCAGCCCGACCGCTGCCGCTTATCCGGTAACTATC 3427

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3395 GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGAGAGCAGATCG
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29.7%; Score 1570; DB 4; Length 4886;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps
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TITLE OF INVENTION: Human Vanilloid Receptor
FILE REFERENCE: 4-30875A
CURRENT APPLICATION NUMBER: US/09/533,220A
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 1.30
SEQ ID NO 4
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; Sequence 4, Application US/09533220A
; Patent No. 6406908
; GENERAL INFORMATION;
; APPLICANT: Mcintyre, Peter
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US-09-533-220A-4
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                                                  2315 GICTIGAGICCAACCCGGIAAGACACGACTIAICGCCACTGGCAGCAGCACCACTGGAAAA 2374
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              GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 3487
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1315 6971090000000000000000000000000000000000	US-08-751-767A-7/c; ; Sequence 7, Application US/08751767A; Patent No. 5994104; GENERAL INFORMATION:

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GCGCCATTTTCCACCATGATATTCGGCAGCAGCATCGCCATGGGTCACGAGGTC 4387
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Pred. No. 0;
0; Mismatches 115; Indels 180;
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTX: USA
COUNTX: USA
COUNTX: USA
COUNTX: DESCONDENCES HIGH
COMPUTER: IBM PC COMPATION
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 117-221
TELEPHONE: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: NUMBER: MINBER: 117-121
TELEPHONE: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: NUMBER: NUMBER: LINGENTHERENTERISTICS:
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TELEPHONE: 7038164100
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Conservative (
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LOCATION: 3222..4841
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STRANDEDNESS: both
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MOLECULE TYPE: cDNA
FEATURE:
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Best Local Similarity
Matches 1849; Conserv
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US-08-751-767A-7
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REPERENCE/DOCKET NUMBER: 2549
TELECOMONICATION INFORMATION:
TELEPHONE: 8015321922
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Pred. No. 0;
0; Mismatches 112; Indels 180;
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Best Local Similarity 86.3%;
Matches 1847; Conservative
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GENERAL INFORMATION:
APPLICANT: White PhD, Kenneth
APPLICANT: White PhD, John
APPLICANT: Reed, William
ITLE OF INVENTION: Cassette for Expression of Lytic
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Trask Britt and Rossa
STREET: P.O. Box 2550
CITY: Sall Lake City
STATE: Utah
COUNTRY: USA
ZIF: 84110
                                                     CTCGCCGTCGGGCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTG
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC comparatible
COMPUTER: ISM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION: 800
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US-08-723-306-6/c
; Sequence 6, Application US/08723306
; Patent No. SE56172...
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NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
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MEDIUM TYPE: Floppy disk
COMPUTER: IBP PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIPTICATION NUMBER: PCT/US96/10041
FILING DATE:
ATOPHEY/AGENT INFORMATION:
NAME: Sweigert PhD, Suean E
REGISTATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATIO
                                                                                                                                                     CGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGGGGGAATCCATCTTGTTCAATCA
GCACAGCTGCGCCAAGGAACGCCCGTCGTGGCCAGCCAACGATAGCCGCGCTGCCTCGTCCT
                                   CTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGC
                                                                                                           DB 5; Length 8797;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11093 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TYPE: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Construct comprising
DESCRIPTION: portions of Bos taurus beta casein gene and genes encor
DESCRIPTION: amphipathic peptide and green fluorescent protein"
HYPOTHETICAL: YES
ANTH-SENSE: NO
FATURE:
NAME/KEY: exon
LOCATION: 1801.1834
Sequence 5, Application US/08723306
Patent No. 5856178
GENERAL INFORMATION
APPLICANT: White PhD, Kenneth
APPLICANT: White PhD, John
APPLICANT: White PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask Bitt and Rossa
STREET: P.O. Box 2250
CITY: Salt Lake City
STATE: Utah
CONDITY: Salt Lake City
STATE: Utah
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURASSIFICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
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NAME/KEY: exon

LOCATION: 3780..3832

OTHER INFORMATION: /product= "beta casein exon 1"

FEATURE:
NAME/KEY: exon

LOCATION: 1766..1773

FEATURE:
NAME/KEY: exon

LOCATION: 4567.4590

OTHER INFORMATION: /product= "portion of beta casein oTHER INFORMATION: (function= "5' flanking regulatory oTHER INFORMATION: /function= "6' flanking regulatory oTHER INFORMATION: /product= "Green fluorescent oTHER INFORMATION: /product= "Green fluorescent"
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OTHER INFORMATION: /product= "beta casein
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                  Length 11093;
                              FEATURE:

NAME/KEY: polyA_signal

LOCATION: 7630._7635

COTHER INFORMATION: /standard_name= "Bovine beta casein
OTHER INFORMATION: 3' region, in exon 9"
US-08-723-306-5
OTHER INFORMATION: /product= "Shiva-1 coding sequence"
                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                          Query Match 29.7%; Score 1569.8; DB 2; Best Local Similarity 86.3%; Pred. No. 0; Matches 1847; Conservative 0; Mismatches 112;
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4092 9830 4152 9770 4212 4272

4332 9590 4392 9530 4452

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ACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA
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NAME/KEY: 5'UTR
LOCATION: 127..1800

OTHER INFORMATION: /function= "5' flanking regulatory
OTHER INFORMATION: region of bovine beta casein gene"
FEATURE:
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LOCATION: 4587..5310
OTHER INFORMATION: protein"
FEATURE:
NAME/KEY: mat peptide
LOCATION: 5320..5449
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LOCATION: 5320..5449
OTHER INFORMATION: /grandard_name= "Bovine beta casein
OTHER INFORMATION: /standard_name= "Bovine beta casein
OTHER INFORMATION: 3' region, in exon 9"
                                                                                                                                                                                                                                                                               Query Match 29.7%; Score 1569.8; DB 5; Length Best Local Similarity 86.3%; Pred. No. 0; Matches 1847; Conservative 0; Mismatches 112; Indels
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1 aagettgaeettatgegaet......tgagtgettgeggeagegtg 5283 Total number of hits satisfying chosen parameters: 2449703 segs, 1841816367 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 US-09-921-143-36 5283 Perfect score: Scoring table: Sequence: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Published Applications NA:*

| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 36, Appl	Sequence 16, Appl		Segmence 16. Appl	Sequence 1. Appli	Sequence 10, Appl	Sequence 11, Appl	Sequence 12, Appl	Sequence 13, Appl	Sequence 14. Appl	15,	Sequence 9, Appli	m	٦,	•
	ΙD	US-09-921-143-36	US-10-198-478-16	US-10-322-360-1	US-10-286-186-16	US-10-038-001-1	US-10-021-403A-10	US-10-395-709-11	US-10-395-709-12	US-10-395-709-13	US-10-395-709-14	US-10-395-709-15	US-10-021-403A-9	US-10-136-837-3	US-09-759-960-7	US-10-128-853-4
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æ	Query Match	100.0	42.4	33.9	32.0	30.9	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.3	29.7	29.7
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ALIGNMENTS

	; Gaps 0;	TCGCTAT 60 TCGCTAT 60	ACTCACG 120 ACTCACG 120	AAAATCA 180 AAAATCA 180
Growth Factor-2	83; DB 13; Length 5283; 0; ches 0; Indels 0;	CTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 	TCAATGGCCGTGGATAGCGGTTTG	TCAATGGGAGTTTGTTTTGGCACC
SULT. 1 -09-921-143-36 Sequence 36, Application US/09921143 Publication No. US20030215921A1 Publication No. US20030215921A1 APPLICANT: Coleman. Timothy TITLE OF INVENTION: Vascular Endothelial Growth Factor-2 FILE REPERENCE: PP112P6 CURRENT APPLICATION NUMBER: US/09/921,143 PRIOR APPLICATION NUMBER: 60/223,276 PRIOR PRILING DATE: 2001-08-04 NUMBER OF SEQ ID NOS: 36 SOFTWARE: Patentin version 3.0 SOFTWARE: Patentin version 3.0 ILENGIH: 5283 TYPE: DNA ORGANISM: homo sapiens -09-921-143-36	100.0%; Score 5283; Similarity 100.0%; Pred. No. 0; 3; Conservative 0; Mismatches	AAGCTTGACCTTATGCGACTTTC	TACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACG	GGGAITTCCAAGTCTCCACCCCACTGACGTCAATGGGAGTTTGTTT
RESULT 1 US-09-21-143-36 Sequence 36, Applicat Publication No. US206 GENERAL INFORMATION: TITLE OF INVENTION: TITLE REFERENCE: PP11 CURRENT FILING DATE: CORRENT FILING DATE: CORPER PARCE: CORRENT FILING DATE: CORPER PARCE: CORRENT FILING DATE: CORRENT FILING DA	Query Match Best Local Similarity Matches 5283; Conser	9y Db	Qy 61 Db 61	Oy 121 Db 121

181 ACGAGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240

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181 ACCAGACTTTCCAAATGTGGTAACAATGCCTTATAAGAGAGAAAAAAGACGTG 300 241 AACATGCTTATTGTGAACGTTGATTACCAAATGCCTTATAAGAGAAAAAAAA

	3661	3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTG 378 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTG 378	3781 GTCATGAGATTATCGTCGACGAAGCGGCCATCCTGCCTCCCCATCCTGCAGTTCGGGG 384 3781 GTCATGAGATTATCGTCGACGAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGG 384	3841	3901 TAGAACTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCG 396 3901 TAGAACTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCCAACTCGCGAGGGATCG 396	Qy 3961 AGCCGGGGTGGGCGAAGAACTCCAGCATGAGATCCCGGGCTGGAGGATCATCCAGCCG 4020	Qy 4021 GCGTCCCGGAAACGATTCCGAAGCCCATCCTTCATAGAAGGCGGCGGTGGAATCGAAA 4080 4021 GCGTCCCGGAAAACGATTCCGAAGCCCTTTCATAGAAGGCGGCGGTGGAATCGAAA 4080	4081	Qy 4141 AGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATAC 4200 4141 AGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGAACGCGCGATAC 4200	OY 4201 CGTAAAGCACGAGAAGCGGTCAGCCCATTCGCCGCAAGCTCTTCAGCAATATCACGGG 4260	OY 4261 TAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCGGCCGCACAGTCGATGAATC 4320	Qy 4321 CAGAAAGGGCCATTTCCACCATGATATTCGGCAGGCATCGCCATGGGTCACGA 4380 Db 4321 CAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCCATCGCCATGGGTCACGA 4380	Qy 4381 CGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGA 4440	OY 4441 GCCCCTGAIGCTCTTCGTCCAGAICAICGACGACAGACCGGCTTCCAICCGAGIAC 4500 1	OY 4501 GTGCTCGCTCGATGCTTTCGCTTGGTGGAATGGGCAGGTAGCCGGATCAAGG 4560	Qy 4561 TÀTGCAGCCGCCACTTGCATCAGCCATGATAGCTTTCTCGGCAGGAGCAAGGTGAG 4620
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Oy 2401 GCAGTGGCACAACTGGGGCGCGGGGGCCGGGGGCAGTGACCTTGGCA		QY 2641 TGGTGCGGGGGAACATGAGTGGGCTGGCTGGCTGGCTGGC	Oy 2701 GCTGTCTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCGGCTCACA	OY 2761 ATTCCACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG	OY 2821 AGCTAACTCA-CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTGGGGAAACCTGTGG	OY 2881 TGCCAGCTGCATTAATGAATCGGCCAACGCGGGGGGGGGG	Qy 2941 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGG	OY 3001 TCACCTCACAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG	CY . 3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGCGG 	Qy 3121 TTTTCCATAGGCTCCGCCCCCTGAGCAGCATCACAAAAATCGACGCTCAAGTCAGAGG Db 3121 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAAATCGACGCTCAAGTCAGAGG	OY 3181 TGGCGAAACCCGACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTGGGG	QY 3241 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTTCGGGA	93 01 AGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGGGGGTCGTTCGCTCGTCGTCGTCGTCGTAGGTCGTTCGCTCGTTCGCTCGTCGTTCGCTCGTCGTTCGCTCGTCG	TCCAAGGTGGGGTGTGCACGAACCCCCCGTTCAGCCCGACGCTGGGGCTTAT	Oy 3421 AACTATCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCTACTTATCGCCACTGGCAGCAGCACTACTATATCGCCACTGGCAGCAGCACTACTATATCGCCACTGGCAGCAGCACTACTATATCGCCACTGGCAGCAGCAACTACTATATATA	3481 GGTAAC

3125 3545 3605 3665 2765 5970 2825 6270 6330 3185 0699 6750 6810 ä 6030 2945 6150 3005 6210 3065 6390 3245 6450 3305 6510 3365 6570 3425 2885 6571 GCTGGGCTGTGTGCACGACGACGACGCTTCAGCCCGACGCTGCGCCTTTATCCGGTAACTA 6630 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTAGTAA 3485 6870 0609

	RESULT 3 10-132-360-1/C US-10-312-360 US-10-312-360-1/C US-10-312-360-1/C US-10-312-360-1/C US-10-312-360-1/C US-20030165946A1 US-2003016946A1 US-2003016946A1
3166 TITTGITTGCAAGCAGCACAATTACGCGCAGAAAAAAAAAA	AGGREGATECTECTECTECTECTECTECTECTECTECTECTECTECT

	; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION ; TITLE OF INVENTION: VECTOR ; FILE REFERENCE: 00801017900USCO ; CURRENT APPLICATION NUMBER: US/10/286,186
13.07 GOSTITICCOLOCCICACCOCCICAGONIACCOCCICACTOCCICCACCICAGONIACOCCICAGONI	agcggccattttccaccatgatattcggcaagcaggcatcgccatgggtcacaa

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TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTA 4326
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                                                                                                                                                             ccdgaagircargacadaAccrccaacacaccaacailiididacacaacaa
                                    -GTCGACCA
                                                                                     AAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATGGATGCGCGGGATAGCCGC
                                                                                                              TGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTCCA
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                                                           --AGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTC
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Pred. No. 0;
0; Mismatches
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/505,477
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                Query Match 32.0%;
Best Local Similarity 82.7%;
Matches 2087; Conservative
                                                                                          TYPE: DNA
; ORGANISM: Porcine Circovirus
US-10-286-186-16
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4145 GGGTCGGCGCGCGGGAAGTCGTCCTCCACGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGGAAGTCCGGAAGTCCGGAAGTCCGGAAGTCCGGAAGTCCGGAAGTCCGGAAGTCCGGAAGTCCGGAATCCGGAATCCGGAATCCGGAATCCGGAATCCGGAATCGAAGTTAATCAAGTCGAACTTAATAAAGCGATTAATCAAGTCGAACTTAATCAAGTCGAATTAATT	4211 GAGGAAGCGGTCACCCATTCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270 3725 GAGGAAGCGGTCAGCCCATTCGCCCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 3666 4271 TATGTCCTGATAGCGGTCCGCCACCCAGCCGCCACGTCGATGAATCCAGAAAGCG 4330 3665 TATGTCCTGATAGCGGTCCGCCACACCCAGCCGCCACAGTCGATGAATCCAGAAAGCG 3606 4331 GCCATTTCCACCATGATATTCGGCAAGCAGCACACAGTCGATGAATCCAGAAAGCG 3606 4331 GCCATTTCCACCATGATATTCGGCAAGCAGCACACGACAGACA	

110	4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCATGGGTCACGACGAGA 4385 2640 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGAGA 2699 4386 TCCTCGCCGTCGGGCATGCGCGCTTGAGCTCGCAACAGCACGAGA 2699 4386 TCCTCGCCGTCGGGCATGCGCGCTTGAGCTTGGCAACAGTTCGGCTGGCGGAGCCC 4445 2700 TCCTCGCCGTCGGGCATGCGCGCTTGAGCTTGGCAACAGTTCGGCTGGCGCAGCCC 2759 4446 TGATGCTCTTCGTCCAGATCATCGACAACAACACTTCCATCCGAGTACGTGCT 4505 2760 TGATGCTCTTCGTCCAGATCATCTGATCGACAACACTTCCATCCGAGTACGTGCT 2819
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TITLE OF INVENTION: UNCERAGED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VITTLE OF INVENTION: US20040014645A1 APPLICAMY: Advisory TITLE OF INVENTION: UNCERAGED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VITTLE OF INVENTION: US20040014645A1 FILE REFERENCE: 10932-0.0115- 4.951-00317- TITLE OF INVENTION: UNCERAGED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VITTLE OF INVENTION: US014-1.015-0.0115- 4.951-00317- TITLE OF INVENTION: UNCERAGED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VITTLE OF INVENTION: UNCERT WELL OF INVENTION: US014-1.015-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.0115- 4.051-0.015-0.015- 4.051-0.015-0.015- 4.051-0.015-0.015- 4.051-0.015-0.0	1892 AAACCCGACAGACTTATAAAATACCAGGCGTTTCCCCCTGGAAGCTCCTCGTGGCGTC 1951

ò	3846 GAIGCGCGGAIAGCCGCTGCTGCTTCCTGGAIGCCGACTTTGCACTGCCGGTAGAA 3905	
Ср	2450 2449	3240 ICAMICALGGGGAAACGAICCIGAICIGITTGAICAGAICTGAICAGAICTGGGGGCGCAI 323
ò	3906 CICCGCGAGGICGICCAGCCICAGGCAGCAGCTGAACCAACTCGCGAGGGGAICGAGGCCC 3965	4986 CAGATICCTTGGGGGGAAGCCATICCAGTTTACTTTGCAGGGGTTTCCAAGGGGTTTACA 3045
QQ	2450 2449	では、またいでは、これでは、これでは、これでは、これでは、これでは、これでは、これでは、これ
ò	3966 GGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTC 4025	
QQ	2450 2449	2000 CONTROL TO THE TOTAL CONT
ò	4026 CCGGAAAACGATTCCGAAGCCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG 4085	
QQ	2450 2449	**************************************
ò	4086 IGAIGGCAGGTIGGGCGICGCTIGGICGGTCAITICGAACCCCAGAGTCCCGGCTCAGAAG 4145	RESULT 9 TG-10-306-700-13
qq	2450CGCTCAGAAG 2459	; Sequence 13, Application US/10395709 ; Publication No. 11820040014645A1
ò	4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAAGCGGGATACCGTAA 4205	GENERAL INFERIOR: APPLICANT: Advisor
qq	2460 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGGCGGCGATACCGTAA 2519	; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE F. TITLE OF INVENTION: GLUTAMARE ("PLG") SYSTEM
& 8	4206 AGCACGAGGAACCGCTCAGCCCATTCCCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265	; FILE REFERENCE: 108328,00115 - AVSI-0021P1 ; CURRENT APPLICATION NUMBER: US/10/395,709 ; CURRENT FILING DATE: 2003-03-24
ò	AACGCTATGTCCTGATAGCGGTCCGCCACACCCGGCCGCCACAGTGAATCCAGAA 4	; NUMBER OF SEQ ID NOS: 25 ; SOFTWARE: Patentin version 3.1
: 名	AACGCTAIGTCCIGATAGCGGTCCGCCACCACCCGCCGCCACACGCCGACAAA 263	; SEQ ID NO 13 ; LENGTH: 3534
ò	4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGA 4385	; TYPE: DNA ; ORGANISM: artificial sequence
q 0	2640 AAGGGGCGTTTTTCCACGATGATATTCGGCAAGCATCGCCATGGTCACGACGAGGA 2699	; FEATURE: ; OWNER INFORMATION: Sequence for the operatively linked components of the TV-GHRH p.
ò	4386 TCCTCGCCGTCGGGCATGCGCCTTCAGCCTGGCGAACAGTTCGGCTGGCCGGAGCCCC 4445	; Olhek infokukilon: Smita. US-10-395-709-13
QQ	2700 TCCTCGCCGTCGGGCATGCGCGCCTTGAGCTTGGCGAACAGTTCGGCTGGCGCAGAGCCCC 2759	Query Match 30.4%; Score 1603.8; DB 12; Length 3534; Rest Local Similarity 82.8%; Pred. No. 0:
δλ	4446 IGAIGCICIICGICCAGAICAICCIGAACGACGACGACTICCAICCAGAIACGIGCI 4505	vative
qq	2760 TGATGCTCTTCGTCCAGATCATCGACAGACCGGCTTCCATCCGAGTACGTGCT 2819	Qy 2706 CTAGACGTAATCATGGTCATAGCTGTTCCTGTGTAAATTGTTATCCGCTCACACAATTCC 2765
λ	4506 CGCTCGAIGCGAIGTTTCGCTTGGTCGAATGGGCAGGTAGCCGGAATCAAGCGTAIGC 4565	Db 1412 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGABATTGTTATCCGCTCACAATTCC 1471
đ	(1)	2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG
à	4566 AGCCGCCATIGCAICAGCCATGATACTITCICGGCAGGAGCAAGAIGAGAIG	1472 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG
<u>ብ</u> ሪ	2880 AGCCGCCGCATTGCATCAGCCATGATACTTTCTCGGCAGGAGGAGAGAGA	OY 2826 ATTCACATTACATTGCGTTGCCCCGCTTTCCAGTCGGGGAAACCTGTCGTGCA 2885
3 8	2940 AGGAGATCCTGCCCGGCACTTGGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 2999	2886
λō	4686 ACGTCGACACACGCCGCAAGGAACGCCCGTCGTGGCCAGCCA	Db 1592 GCTGCATTAATGAATGACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC 1651
qq	3000 ACGTCGAGCACCAGCTGCGCAAAGGAACGCCCGTCGTGGCCACGATAGCCGCGCTGCC 3059	Qy 2946 GGCTTCCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGCGAGCGA
ò	4746 TCGTCCTGCAGTTCATTCAGGCACACCGGACAGGTCTTGACAAAAAGAACCGGGCGC 4805	Db 1652 CGCTTCCTCGCTCACTCGCTCGCTCGTTCGGCTGCGGCGAGCGGTATCAGC 1711
qq	3060 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTTTGACAAAAAAAA	
λŏ	CCCTGCGCTGACAGCCGGAACACGGCGGATCAGAGCAGCCGATTGTCTGTTGCCCAG 4	
g :	CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCTGATTGTCTGTTGTGCCCAG 3	OY 3066 GTGAGCAAAAGGCCAGGAAAAGCCCAGGAAAAGGCCGCGTTGCTGGCGTTTTT 3125
S 8	3180 TCATAGCCGAATAGCCTCTCCACCCAAGGGGGGAAAACTGCGGGCAATACCATTGT 3239	3126 CCATRAGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG

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GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATG 3845
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                                                                                                          TITITETTTGCAAGCAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT
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                                                                                        TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT
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     CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT
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CRGANISM: artificial sequence
FEATURE:
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US-10-395-709-14
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Best Local Similarity 82.8%;
Matches 2022; Conservative
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version
SEQ ID NO 14
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Db 1592 GCTGCATTAATGAATCGGCCAACGGGGGGAGGGGGTTTGCGTATTGGGCGCTCTTC Qy 2946 GGCTTCCTCGCTGACTGGCTTCGGCTGGCGGGGGGGGGG		Qy 3166 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTTT	Qy 3126 CCATAGGCTCCGCCCCCTGAGGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG D 1832 CCATAGGCTCCGCCCCTGAGGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG	3186	32461	Qy 3306 GGGGTTTCTCATAGGTCATGGTAGGTATCTCAGTTCGGTGTAGGTAG	3366	OY 3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCAGCTGGTAA	THE POL Db 2192 CAGGATTAGCAGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGCTAA THE POL Db 2192 CAGGATTAGCAGAGGGTATGTAGGGGGTGCTACAGAGTTCTTGAAGTGGTGGTGCTAA	OY 3546 CTACGGCTACACTAGAAGAACAGTAITTGGTAICTGCGCTCTGCTGAAGCCAGTTAACTTT	Oy 3606 CGGAAAAAGACTTGGTAGCTCTTGATCCGGCAAACAACACGCTGGTAGCGGTGGTTGTTTTTTTT	Oy 3666 TITIGITIGCAAGCAGAGTTACGCGGAGAAAAAAAAGATCTCAAGAAGATCCTTTGAT	Qy 3726 CTITICTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT	QY 3786 GAGATTATCGTCGACCAAGGGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATG	Db 2450	2450	dy 3906 CTCCGCGAGGTCGTCCAGCCTCAGGCAGCTGAACCAACTCGCGAGGGGATCGAGCCCC	Qy 3966 GGGGTGGGGAAGAACTCCAGCATGAGATCCCCGGCGCTGGAGGATCATCCAGCCGGCGTC
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                                 3420 AACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT 3460
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5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT
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TITLE OF INVENTION: Administration of Nucleic Acid
FITLE OF INVENTION: Growth in Offspring
FILE REPRENCE: HO-POZO21US1/100021476/OTA 00-91
CURRENT APPLICATION NUMBER: US/10/021,403A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION WIMBER: 60/255,021
PRIOR PILLNG DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1603.8;
Pred. No. 0;
0; Mismatches
                                                                                                                   ; Sequence 9, Application US/10021403A; Publication No. US20030074679A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.8%;
Matches 2022; Conservative (
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SEQ ID NO 9
LENGTH: 3534
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                                                                                   RESULT 12
US-10-021-403A-9
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                                                                                 TGATGGCAGGTTGGCCTTGGTCGGTCATTTCGAACCCCCAGAGTCCCGGCTCAGAAG
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1,000	RESULT 13 US-10-136-837-3 US-10-136-837-3 Sequence 3, Application US/10136837 Publication No. US20030181405A1 GENERAL INFORMATION: APPLICANT: PERICLE, Federica APPLICANT: ROLLAND, Alain APPLICANT: ROLLAND, Alain APPLICANT: RALSTON, Robert TITLE OF INVENTION: Interferon Alpha Plasmids and Delivery Systems, and Methods of TITLE OF INVENTION: Using the Same FILE REPERENCE: 273/082 (GM15-1USC1) CURRENT RILING DATE: 2002-04-29 FRIOR APPLICATION NUMBER: US/10/136,837 CURRENT RILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Patentin version 3.1 SEQ ID NO 3 LENGTH: 5966 TYPE: DNA
3366 GGGCCTTTCTCATAGCTCACGCTGTAAGTACTCAGTTCGGTAAGTCGTTCGCTCCAA 3365	4086 TCCTCGCCGCTCGCTTGGTCGCTCTTTCGAACCCCAGAGTCCCGCTCAGAAG 4145 2450 4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCAGAAG 2459 4146 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 4205 2450 AACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAA 2519 4206 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATACCGCGATACCGTAA 2519 2520 AGCACGAGGAAGCGGTCAGCCCATCGCGCCAAGCTCTTCAGCAATACCAGGGTAGCC 2579 4266 AACGCTATGTCCTGATAGCCGTCACCCCAGCCGGCCAAGTCCATGAATCCAGGATAGCC 2579 4266 AACGCTATGTCCTGATAGCGGTCGCCACACCCAGCCGGCCAAGTCGATGAATCCAGGA 4325 2580 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCAAGTCGATGAATCCAGAA 4385 2540 AAGGCGCCATTTTCCACCATGATATTCGGCAAGCCATGACTCAAGAACGAAGAA 2639 4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCATGACCAAGAA 2639 4326 AAGCGGCCATTTTCCACCATGATATTCGGCAAGCATGCCATGGGCGAAGAA 2639 4386 TCCTCGCCGTCGGGCAAGCCTTGAGCCTGGCGAAGCACCCCAAGGCTCGCCAAGGCTCGCCAAGACAAGAACCCCAAGACAAGAACCCCAAGACAACA

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e 12 pIN0961	Obery Match 30.3%; Score 1600; DB 13; Length 5966; Best Local Similarity 83.5%; Pred. No. 0; Matches 2005; Conservative (), Mismatches 5; Indels 392; Gaps 1; Ov. 2706; Chadancancancancancancancancancancancancanca	60 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCC	OY 2.75 ACACAACATACAACACAAAAGTGTAAAGCCTGGGGGTGCCTAATGAGTGAG	OY 2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885	OY 2886 GCTGCATTAATGAATGGGCCAACGCGGGGGAGGGGGGTTTGGGTATTGGGGCGTCTTC 2945	Oy 2946 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTTCGGCTGCGGCGGAGCGGTATCAGC 3005	3006 TCACTCAAAGGGGTAATACGGTTATCCACAGAATCAGGGGTAACGCAGGAAAGAATCTAGGGGATAACGCAGGAAAGAATCAGGGGATAACGCAGGAAAACATCACACACA	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 	TGGCG 31	OY 3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245	TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAGCGTTCCCTTCGGGAATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTTCCTCCTTCGGGAAGCGTTCCCGCCTTCCGGGAAGCGTTCCGGCTTCGGGAAGCGTTCCGGCTTCGGGAAGCGTTCCGGAATACCTGCCGGCTTTCCCGGGAAGCGTTCCGGAATACCTGCCGGCTTTCCCGGGAAGCGTTCCGCCTTCGGGAAGCGTTCCGCCTTCGGGAAGCGTTCCGCCTTCGGGAAGCGTTCCGCCTTCGGGAAGCGTTCCGCCTTCGGGAAGCGTTCCGCCTTCCGGAAGCGTTCCGCCTTCCGGAAGCGTTCCGCCTTCCGCCTTCCGGGAAGCGTTCCCGCCTTCCGCCTTCCGGAAGCGTTCCCTTCCCGCCTTCCGGAAGCGTTCCCTCCC	CCAA	AACTA ACTA ACTA ACTA	TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCAGTGGTAA TCGTCTTGATCCAACCGGGAAGAAGAAGAACAACGACTTGAACAAGCAAG	3486 CAGGATTAGCAGAGGTATGTAGGGGGTGCTACAGAGTTCTTGAAGTGGGGCCTAA	3546	3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACGCTGGTAGCGGTGGTTT

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Query Match
Best Local Simi
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                                                              1768 CCCTGCGCTGACAGCCGGAACACGGCGCATCAGAGCAGCCGATTGTCTTGTTGTTGTTGTCCCAG
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                                             CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG
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US-09-759-960-7/C

Sequence 7, Application US/09759960

Sequence 7, Application US/09759960

Sequence 7, Application US/09759960

Secont No. US20010006639A1

APPLICANT: Urban, Robert G.

APPLICANT: Chicz, Roman M.

APPLICANT: Collins, Edward J.

TITLE OF INVENTION: IMMUNOCENIC PEPTIDES FROM THE HPV

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES. 33

CORRESPONDENCE ADDRESS:

ADDRESSE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: BOSCON

STREET: 225 Franklin Street

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATION STREET: US/09/759,960

FILING DATE: PROTEIN UNDER: US/09/759,960

FILING DATE: RASALICATION DATA:

APPLICATION NUMBER: 09/169,425

FILING DATE:

ATORNEY/AGENT INFORMATION:

NAME: FISSENCE/DOCKET NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 34,819

TELLERAN: ACTIVE ATTORN NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 34,819
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TELEX: 201154
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
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                                                                                                                                             2624 AATGCATGCGGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT
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                                                                                                                                                                                                                                                                                                                          ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA
                                                      Gaps
Score 1571.6; DB 9; Length 4665;
Pred. No. 0;
); Mismatches 114; Indels 180;
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                                                 0;
29.7%;
                                                    Conservative
                            Similarity
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Qy 4928 AATCATGCGAAACGATCCTCATCTTTGATCAGATCTTG 4971	PRESENT PRES	
3947 TCGCGAGGGATCGA 3961 	1544 TCMIAGGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAGTNAGCTCCCCCTCWG 1465 1544 TCMIAGGCGGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAGTNAGCTCCCCCCTCCGGTAG 1446 GGTGGGCGGGTTCCTTCCGTATTCGTTCGTTCGGTGTTCCTCCCCCCTCGGTAG 1454 GGTGGGCGGGTTCCGTATCGTATCCCCCTCGGGGTTCCCCCTCGGTAG 1454 GGTGGGCGGGTTCCGAACCCCATTCGAACCCCGCTGGGGAATTCCGAACCCCCTCGGTAG 1454 GGTGGGCGGGTTCGAACCCCATTCGAACCCGCGTGGAAATTCCCACGAACCCGCTTCGAACCCGCTGGGGGTTCCCCTCGAACGCGGGTTCCCCTCGAACGCGGGGTTCCCCTTGAACCCGCGTGGGGAATTCCGAACCCGCTTCGAACCCGCTTGGGAACCCGCCTCGAACGCGGGGTTCCGAACCCGCTTGGAACCCGCTTGGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCCCTCGAACGCGGTTGGAACCCGCTTCGAACCCGCCCCCTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCGCTTCGAACCCCCTTCGAACCCCCTTCGAACCCCCTTCGAACCCCCTTCGAACCCGCTTCGAACCCGCTTCGAACCCCCTTCGAACCCCCCTTCGAACCCCCTTCGAACCCCCTTCGAACCCCCCTTCGAACCCCCCTTCGAACCCCCCCC	

Db 2615 CTCGATGCGATGTTTCGCTTGGTGGATCGAATGGGCAGGATCAAGCTATGCAG 2556 4568 CCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAG 4627 Db 2555 CCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGACAG 4627 Qy 4628 GAGATCCTGCCCGGCACTTGGCCAATAGCAGCCAGCAGCAGGAGCAAGGTGACAAG 2496 Qy 4628 GAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCCTTCAGTGACAAC 4687 Db 2495 GAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCCTTCAGTGACAAC 2436 Qy 4628 GTCGAGCACAGCTGCCCAAGAAACGCCCGTTCAGTGACAAC 2436 Qy 4628 GTCGAGCACAGCTGCCCAAGAAACGCCCGTCTCGCTTCAGTGACAAC 2436 Qy 4688 GTCCTGCAGTTCATTCAGGCACCCGTCGTGGCCAGCAGCCCCGCTTCAGTGACAAC 2436 Qy 4748 GTCCTGCAGTTCATTCAGGCAACGACGAGCCGCCCGAGTAGCCGGCCCCCCGTGCCTC 2376 Qy 4808 CTGCGAGTTCATTCAGGCAACGACAGGTCGGTCTTGACAAAAAAAA	4868 ATAGCGAATAGCCTCTCCACCC 2255 ATAGCGAATAGCCTCTCCACCC 4928 AATCATGCGAAACGATCCTCATC 195 AATCATGCGAAACGATCCTCATC	Search completed: February 15, 2004, 10:50:34 Job time : 1750 secs				_						
	CGTATTATGAACAAAACGACCAACGTTTTATTATTATTATTATTGCCG	3962GCCCGG 3967 3215 TCATAGCGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAGTTAGCCTCCCCTAG 3156	GGTGGGCGAAGAACTCCAGCATGAGATCCCCGGCCTGGAGGATCATCCAGCCGGGGTCCC	4028 GGAAARCGATTCCGAAGCCCAACCTTTCATAGAAGGCGGGGGGGAATCGAAATCTCGTG 4087 	4088 ATGGCAGGTTGGGCGTCGCTTGGTCGGTCGTTTCGAACCCCAGAGTCCCGCTCAGAAGAA 4147 	4148 CTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGGGGTACCGTAAAG 4207 	4208 CACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267 	4268 GGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACACTCGATGAATCCAGAAAA 4327 	4328 GCGGCCAITITCCACCAIGAIAITCGGCAAGCAGGCAITGCCAIGGGTCACGAGAGAGAIC 4387 	4388 CTCGCCGTCGGGCATGCGCGCTTGAGCCTGGCGAACAGTTCGGCTGGCGGCGAGCCCGTG 4447	4448 AIGCICITICGICCAGAICAICAIGACAAGACGGGCTICCAICCGAGIACGIGGTCG 4507	4508 CTCGATGCGATGTTTCGCTTGGTGGAATGGGCAGGTAGCCGGATCAAGCGTATGCAG 4567

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AU081044 AU081.044
BZ572294 MRD12.5572
BG680319 MRD12.5572
BG680319 MRD12.5572
BZ686412 BHO1D.047
ALO44364 DKFZ04434C
BZ579291 MRD2.6285
BZ574513 MRD2.6285
BZ574513 MRD2.6285
BZ574513 MRD2.6285
BZ574513 MRD2.6276
BZ57989 BRC2.6095
AU571166 ARADIGOPS
AU571166 ARADIGOPS
AU571166 ARADIGOPS
BZ557989 BRC2.6095
AU571166 ARADIGOPS
BZ57981 MRD.67114
AZ681169 ARADIGOPS
BZ57981 AL959357
BZ570648 MRD2.1469
BZ557981 AL959357
BZ570648 MRD2.1469
BZ57391 MRD2.1469
BZ57391 MRD2.1950
AL051420 AL661706
BZ57391 MRD2.1950
AL061706 AL661706
BZ57391 MRD2.1950
AL05168 AL65668
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK047844 linear HTC 05-DEC-2002 MRNA linear HTC 05-DEC-2002 Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30004W09 product:vascular endothelial growth factor C, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
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DEG80919
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BZ570648
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AK047844.1 GI:26339001
ATC: CAP trapper.
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AK047844
LOCUS
DEFINITION
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AUTHORS
TITLE
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AU081137 AU081137
AU081124 AU081124
CB686151 BN01b_020
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(without alignments)
12887.739 Million cell updates/sec
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itch,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Arakawa,T., Hara,A., Fukunishi,Y., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Gaito,T., Gaito,T., Caito,T., Caito,T., Caito,T., Casto,T., Casto,T., Casto,T., Casto,T., Casto,T., Rachan,M., Gasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Marsuo,Y., Nikaido,I., Fesole,G., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Fletcher,C., Fullta,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Kohtsuki,S. and Hayashizaki,Y. Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y. Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. Puctional annotation of a full-length mouse cDNA collection of the collection
                                                Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sawi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahki, M., Okacaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384 format Genome Res. 10 (11), 1757-1771 (2000)
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas.

Mature 420, 563-573 (2002)

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Redchi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Roth,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Kawai,G., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,R., Ohno,M., Ohsato,N., Okaano,H., Sakai,C., Sakai,K., Saito,R., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shikat,R., Shikat,R
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Direct Submission
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1081 TCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATG 1140

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Please visit our web site for further details

URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/ Location/Qualifiers

FEATURES

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/trānslation="MHILCFLSLACSLIAAALIPSPREAPATVAAFESGLGFSEAEPD
GGGSVKAPSGKDLEBQLASVSSVDELMSYLYPDYKKYKCGLAKGGWQPTLNTRTGDS
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PGLSFSEEVCRCVPSYWKRPHLN"
                                                                                                                                                                                                                    /tissue_type="head"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="16 days embryo"
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/note=unnamed protein product; putative
/note=unnamed protein product; putative
delunamed protein product; putative
GB|NM_009506, evidence: BLASTN, 99%, match=1784)"
/codon start=1
/protein id="BAC33172.1"
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0; Mismatches 180; Indels
                                                                                                      |db xref="FANTOM DB:C130004M09"
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Best Local Similarity 85.4%;
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FEATURES 11067 Source 11067 /organism="noncorhynchus mykiss" /mol type="mRNA" /db zxef="texon:8022" /clone="K12" /tissue type="kidney" /clone="K12" /clone="K12" /clone="Locothynchus mykiss Kidney infected by . /clone="common name:rainbow trout; infected by . hematopoietic necrosis virus" /note="common name:rainbow trout; infected by infectious hematopoietic necrosis virus" Note="common name:rainbow trout; infected by infectious hematopoietic necrosis virus" Note="common name:rainbow trout; infected by infectious hematopoietic necrosis virus" BASE COUNT 235 a 292 c 288 g 250 t 2 others	Query Match 17.9%; Score 948; DB 9; Length 1067; Best Local Similarity 98.8%; Pred. No. 4.2e-254; Matches 976; Conservative 0; Mismatches 10; Indels 2; Gaps 2; Qy 2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765 Db 82 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCGGCTCACAATTCC 141		262 GCTGCATTAATGAATCGGCCGGGGGGGGGGGGTTTGCGTATTGGGCGCTTTC 321 2946 CGCTTCCTCGCTCACTGACTCGCTCGCTCGTTCTCGCTGCGCGGGGGGGG	0y 3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATAACGGAGGAAAGAACAT 3065	Db 502 CCAITAGGCTCCGCCCCCCGAACAACACCCCCAACACCCCCAAGCTGGCG 561 Oy 3186 AAACCCGACCACCCCCCCCAGCGTTCCCCCCTGGAAGCTCCCCTGGCGCTC 3245 Db 562 AAACCCGACCAGACTATAAAGATACCAGCGTTTCCCCCTGGAAGCTCCTCGTGCGCTC 621 Oy 3246 TCCTGTTCCGACCCTTACCGGATACCTGCCCCTTCGGAAGCTCCTCGGGAAGCGT 3305 Db 622 TCCTGTTCCGACCCTTACCGGATACCTGCCGCTTTCTCCCTTCGGGAAGCGT 681 Oy 3306 GGCGTTTCTCATAGCTCACGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 681 Oy 3306 GGCGTTTCTCATAGCTCACGGTTACCTGTCCGCTTTCTCCCTTCGGGAAGCGT 741 Oy 3366 GGCGTTTCTCATAGCTCACGGTTACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT 681 Oy 3366 GGCGTTTCTCATAGCTCACGGTTACTCAGTTCGGTTAGGTCGTTCGCTCCAA 741 Oy 3366 GTGGGCTTTCTCATAGCTCACGGTTACTCGGTTAGGTCGTTCGGTTACTTAC
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QY 2946 CGCTTCCTCGCTCACTGACTCGCTGCGTCGTTCGGCTGCGGCGGGGGGGTATCAGC 3005 Db 323 CGCTTCCTCGCTCACTGACTCGCTGCGTCGGTTCGGCTGCGGCGGAGCGGTATCAGC 3005 QY 3006 TCACTCAAAGCGGTAATACGGTTATCCACAGAATACGCAGGAAAGAACAT 3065 Db 383 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 442 QY 3066 GTGACCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTTTTT 3125 QY 3066 GTGACCAAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTTTTT 502 QY 3126 CCATAGGCTCCGGCCCCTGACGGAACCGTAAAAAAGGCCGCGTTTTTTTT	Oy 3186 AAACCCGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCTCGTGGGCTC 3245	3366 GCTGGGCTGTGTGCACCACCCCGTTCAGCCCGGCCGCTGCGCCTTATCCGGTAACTA	Db 923 ACTACGGCTACATAGAACAGTATTTGGATATCGGGGGTCGGGGGGGG		ORGANISM Brassica napus ORGANISM Brassica napus Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids ; eurosids II; Brassicales, Brassicaceae, Brassica. REFERENCE 1 (bases 1 to 925) AUTHORS Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A., Chagnon,J., Farah,S., Couroux,P. and Hattori,J. TITLE Expressed Sequence Tags from constitutively frost tolerant transcentc Brassica napus overexpressing BNCBE17
Qy 3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605 Db 922 CTACGGCTACACTAGAAGACACTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 981 Qy 3606 CGGAAAAAAGAGTTGGTACTCTGATCCGGCAACCAACACACCGCTGGTAGCGTTT 3665 Db 982 CGGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAAAACAAAC	LOCUS AU081124 AU081124 DEFINITION AU081124 DEFINITION AU081124 ACCESSION AU081124 ACCESSION AU081124.1 GI:6431472 KEYWORDS SOURCE ORCANISM ORCATYANCHUS mykiss (rainbow trout) ORCANISM ACCESSION AU08124.1 GI:6431472 COCOTHYNCHUS mykiss SOURCE ORCATYANCHUS mykiss COCOTHYNCHUS mykiss Actinopterygii; Plebstei; Euteleostomi; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	REFERENCE 1 (bases 1 to 1089) AUTHORS KONO,T., Sakai,M. and LaPatra,S.E. TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious Hematopoletic Necrosis Virus JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001) COMMENT Conteact: Masahiro Sakai Faculty of Agriculture Miyazaki university 1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan Email: m.sakai@cc.miyazaki-u.ac.jp.		Query Match 17.4%; Score 919.8; DB 9; Length 1089; Best Local Similarity 97.2%; Pred. No. 3.5e-246; Indels 6; Gaps 4; Matches 979; Conservative 0; Mismatches 22; Indels 6; Gaps 4; Qy 2706 CTAGACGTAATCATGGTCATAGCTGTTCCTGTGTGAAATGTTATCGGCTCACAATTC 742 Db 83 CTTGGCGTAATCATGGTCATAGATGTTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGAGTGAATTC 142 Qy 2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAAGCCTGGGGTGCCTAATGAGTGAG	Qy 2826 ACTCACATTAATTGCGTTGCGCTCACTGCCGGGAAACCTGTCGTGCCA 2885 Db 203 ACTCACATTAATTGCGTTGCCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 262 Qy 2886 GCTGCATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTTGCGTATTGGGTCTTC 2945 Db 263 GCTGCATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTTGCGTATTGGGTCTTC 322

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Class: shotgun.
Location/Qualifiers
1. .966
/organism="Pseudomonas i/mol_type="genomic_DNA"
/strain="MSH"
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          Contact: Singh,J.A.

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Email: singhja@em.agr.ca.
Location/Qualifiers
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966 bp DNA linear GSS 17-DEC-2002 msh2 1513.x1 msh Pseudomonas aeruginosa genomic clone msh2_1513, pgenomic survey sequence. 3420 2949 3009 3010 TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA 3069 3421 AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACT 3480 3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540 AACTATGTCTTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGSAGCAGCCACT 120 3599 3 299 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 240 TCCAAGCTGGGCTGTGCACGAACCCCCGTTCAGCCCCASCGCTGATCCGGT 180 153 213 Gammaproteobacteria; Pseudomonadales; CATTAATGAATCGGCCAACGCGGGAGAGGGGGTTTGCGTATTGGGCGCTCTTCCGCT 2890 CATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT 2950 ICCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGGCGGTATCAGCTCAC CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGT CTTAACTACGGSTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGT /db_xref="taxon:287"
/clone="mmA2 1513"
/clone lib="mmhz is"
/note="Environmental isolate. Whole genomic shotgun Pecudomonas aeruginosa
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Pecudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonada
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonada
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonada
Bacteria; Pseudomonas.

Spencer, D.H., Ravund, C.K., Smith, E.E., Sims, E.E., Hastings
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press οŧ 7 15.3%; Score 809.2; DB 29; Length llarity 97.0%; Pred, No. 3.7e-215; Conservative 0; Mismatches 24; Indels others aeruginosa" USA u Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, Tel: 2062216954 Fax: 2066857244 209

Miyazaki University 1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan Email: m.sakai@cc.miyazaki-u.ac.jp. Location/Qualifiers 1 . 1163	ORIGIN Query Match Best Local Similarity 99.5%; Pred. No. 3.1e-207; Matches 794; Conservative 0; Mismatches 3; Indels 1; Gaps 1; Qy 2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTGTTATCGGCTCACAATTCC 2765 Db 367 CTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCGCTCACAAATTCC 2765		Qy 2946 CGCTTCCTCGCTCACTGACTGCGCTCGGTCGTTCGGCTGCGGGGGGGG	3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGGTTGCTGGCGGCTTTTTTTT	Db 847 AAACCCGACACAGACTATAAAGATACCAGGCGTTTCCCCCTGGAGGCTCCTCGTGGGGGGTCTCTCTC	3366 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 1027 GCTGGGCTGTGTGCACGAA-CCCCGTTCAGCCCGACGCTGCGCTTTTATCCGGTAACTA 3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGGAAA 1086 TCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGGAAA 1086 TCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCACCACTGGTAA
Db 214 TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGGATAACGCCAGGAAAGAACATGTGA 273	Db 454 GTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCG 513 Qy 3310 CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTGTAGGTCGTTCGCTCCAAGCTG 3369 Db 514 CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGAGGTTCGCTTCAAGCTG 573 Qy 3370 GGCTGTGTGCACGGTGTAGGCCCCACCGGTGCGTTATCCGGTAACTATCGT 3429	3430 CTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCACTGGTAACAGG 634 CTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCACTGGTAACAGG 3490 ATTAGCAGAGCAGCTATTGGCGACTTATCGCCACTGGAGCAGCACTAGAGAGG 694 NATAGCAGAGCAGTATTGGCGAGTACTACAGAGTTCTTGAAGTGGTAGCTACAGG 694 NATAGCAGAGCAGTATTTGGTAACAGAGTTCTTGAAGTGGTAGCTAACTAC 696 NATAGCAGAAGAAGAATTTTGGTATCTGCGCTCTGAAGCCGATTACCTACGA	Db 754 GGCTACACTAGAAGAACAGTATTTGGAACCTGCGCTCTGCTGAAGCC-GGTACCTTCGGA 812 0 0 0 0 0 0 0 0 0	OY 3730 TCTACGGGGTCTGACGCTCAGTGGAAGAAA 3760	hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KB1, mRNA sequence. ACCESSION AU081044 VERNORDS SET. AU081044.1 GI:6431392 KEYWORDS SET. ONGORNED ONCORHYNCHUS mykiss (rainbow trout) ONGANISM ONCORHYNCHUS mykiss Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi; Actinopteryoti; Neopteryoti; Teleostei; Buteleostomi;	REFERENCE 1 (bases 1 to 1163) AUTHORS Kono.T., Sakai, M. and LaPatra, S.E. TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncortynchus mykiss) Infected with Infectious Hematopoletic Necrosis Virus JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001) Contact: Masahiro Sakai Faculty of Agriculture

3482

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 831)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CONTACT: Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC cloud distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov.
Plate: LiAMIO613 row: o column: 04
High quality sequence stop: 810.
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602628716F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4753755 5',
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  CTCTCCTGTTCCGACCCTGCCGCTTACGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAG
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/lab.host="DHIOB (TI phage-resistant)"
/clone lib==NOI GCAP Skr4"
/note="Organ: skin, Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                  CTATCGTCTTGAGTCCAACCCGGTAAGACACACTTATCGCCACTGGCAGCAGCCACTGG
                                                                                                                                                                                                                                                                                                                                           700 TAACAGGATTAGCAGAGAGCGAGGTATGTAGGCGGGGCTACAGAGTTCTTGAAGTGGTGGCC
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/db_xref="taxon:9606"
/clone="IMAGE:4753755"
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                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria, Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 1249)
Spencer, D. H., Raymond, C.K., Smith, B.E., Sims, B.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
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/done="mmh2_2572"
/clone_lib="mmh"
/note="Environmental isolate. Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 781.2; DB 29; Length 1249;
Pred. No. 3.2e-207;
0; Mismatches 35; Indels 6;
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    1249
    forganisma-"Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"

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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066216954
Email: Graymond@u.washington.edu
Class: shotgun
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                          1146 CAGGATTAGCAGAGCGAG 1163
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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HWE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /done lib= MADPCL"
/clone lib= MADPCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Pinter limits method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 858)
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: Gapabs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Plate: LLAM14279 row: 1 column: 15
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                                                                                                                                                                                                                                                                   NIN-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                         Homo sapiens (human)
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CA488579
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."

223 c 238 g 182 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3061 AACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAAGAACCGTAAAAAAGGCCGCGTTGCTGGCG 3120
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                                                                                                                                                                                                                                                                                         812 GCGCGCTTGGCCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACA 753
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DKFZp434C172_s1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434C172 3', mRNA sequence.
                                                                                                                              Similarity 99.0%; Pred. No. 3.6e-207; Similarity 11, Mismatches 5; Indels 2;
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/tissue_Type="fourth leaf"
/tissue_type="fourth leaf"
/dev_stage="3" weeks seedling grown at room temperature"
/clone_lib="Bnoib AAPC ECORC transgenic Brassica napus_ove_
rexpressing_BNOBF17 constitutively_frost_tolerant"
/note="voetcr: Bluescript SK+/KNoIT Steel: BcoxI;
/note="voetcr: Bluescript SK+/KNoIT Steel: BcoxI;
/steel: XnoI; Germinated in soil flats and seedlings grown
for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                                                                                                                        1363 GATGAAGAGCTGTCAGTGTGTCTGCAGAGCGGGGTTTCGGCCTGCCAGCTGTGGACCC 1422
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Bnolb_04fC_ECORC transgenic Brassica napus overexpressing BNCBF17 c
onstitutively_frost_tolerant Brassica napus cDNA clone BnOlb_04j14,
mRNA sequence.
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Brassica napus (rape)
Brassica napus
Brassica napus
Brassica napus
Brassica viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
i eurosids II; Brassicales; Brassicaceae; Brassica.
(bases 1 to 833)
Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
Expressed Sequence Tags from constitutively frost tolerant
transgenic_Brassica napus overexpressing BNCBF17
                    1303 GAIGCIGGAGAIGACICAACAGAIGGAITCCAIGACAICTGIGGACCAAACAAGGAGCIG 1362
                                                                                                                                                                                                                             TGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCA 1602
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                                                   481 GATGAAGAACCTGTCAGTGTGTGTGTGGGGGGTTTCGGCTGCTGCTGTGGACCC 540
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Westar"
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Location/Qualifiers
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(613) 759-1701
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Oy 3367 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACC Db 661 CTGGGCTGTGTGCACGAACCCCCGGTTCAGCCCGAAC OY 3427 CGTCTTGAGTCCAACCGGTAAGACACGGTTATCGC Db 721 CGTCTTGAGTCCAACCCGGTAAGACACTTATCGC OY 3487 AGGATTAGCAGAGCGATGTAGCGGTTGTATCG OY 3487 AGGATTAGCAGAGCGTTGTAGCGGTGTACACCTATCGAGCGTTATCGCGGTGTAGAGCGGTTATCGCGGTAGAGCGGTTATCACAGAGCAGAGCTATGTAGAGCGGTGTACACACAGCGTATCACACAGCGAGCTATCACACAGCGAGCTATCACACAGCGAGCTATCACACACA	9011 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	NEFERENCE I CLASSES A.C. A.S. AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.B. BUTHORS Burns, J.L., Kaul, R. and Olsen, M.V. TITLE Whole-Genome-Sequence variation among Psedomonae aeruginosa library JOURNAL Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, US Fax: 206685744		BASE COUNT 327 a 356 c 351 g 334 t ORIGIN Query Match Best Local Similarity 95.6%; Pred: No. 1.5e-1 Matches 797; Conservative 0; Mismatches Qy 2840 CGTTGCGCTCACTGCCCGTTTCCAGTCGGAAACC Qy 2900 CGGCTCACTGCCCGTTTCCAGTCGGAAACC Qy 2900 CGGCCAACGCGGGGGAGAGGGGGATTGCGTATTC Qy 2900 CGGCCAACGCGGGGGGAGAGGGGGTTTGCGTATTC Qy 2900 CGGCCAACGCGGGGGGAGAGGGGGTTTGCGTATTC Qy 2900 CGGCCAACGCGGGGGGGGGGGTTTGCGTATTC Qy 2900 CGGCCAACGCGGGGGGGGGGGGTTTGCGTATTC Qy 2900 CTGACTCGCTGCGGGGGGGGGGGGGTTTGCGTATTC Qy 2900 CTGACTCGCTGCGGGGGGGGGGGGTTTGCGTATTC Qy 2900 CTGACTCGCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGG
	Contract: Ansorge w MVES Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany Infisia the 3' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, Germa Clone from S. Wiemann, Molecular Genome Analysis, Germa Research Center (DKFZ); Email s.wiemann@dkfz-heidelber Sequenced by EMEL (European Molecular Biology Laborator Heidelberg/Germany) within the cDNA sequencing consorti German Genome Project. No Is equence available at the RZPD in B Please contact the RZPD: Ressourcensentrum, Heubnerweg Phis clone (DKFZP4340172) is available at the RZPD in B Please contact the RZPD: Ressourcensentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. 1. 954	/note=Vector: pSport1; Site_1: Not1; Site_2: SalI" 214 a 273 c 253 g 214 t .tch 14.7%; Score 774; DB 9; Length 954; 774; Conservative 0; Mismatches 0; Indels 0; Gaps 1887 CTGCATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGCGCTCTTCC	2947 GCTTCCTCGCTCACTGACTCGCTCGCTCGGTCGGCTGCGGCGGCGACGCTTCAGCT 3006 241 [3127 CATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA 3186 421 CATAGGCTCCGCCCCCTGACGAGGACATCACAAAATCGACGCTCAAGTCAAGGTGGCGA 480 3187 AACCCGACAGGACTATAAAGATACCAGGCTTTCCCCTTGGAGTTGCCTTT 3246 481 AACCGGACAGGACTATAAAATACTTCCCTTGGAGTCCCTTCGTGGGTTT 540 3247 CCTGTTCCGACGCTTTAAAAATTCCAGGATACTGTCCCTTCGTGGGCTCT 540 521 CCTGTTCCGACGCTTTACCGGATACTGTCCCCTTCTCGCGAAGCGTG 3306 541 CCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCCCTTCTCGCGAAGCGTG 600 5307 GCGCTTTCTCATAGGTCACGGTTACCGGTAAGGTTCGCTCCCAAG 3366 601 GCGCTTTCTCATAGCTCACGGTAAGTATCTCAGTTCGGTAAGGTTCGCTCCAAG 600 601 GCGCTTTCTCATAGCTCACGGTAAGGTATCTCAGTTCGGTAAGGTCGTTCGCTCCAAG 600
KEYWORDS SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL	PEATURES SOUICE	BASE COUNT ORIGIN Query Ma Best Loc Matches Qy 2	90 90 90 90 90 90 90 90 90	8 5 8 5 8 5

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AGCGGTATCAGCTCACTCAAAGGCGG 3019
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CCGCTGCGCCTTATCCGGTAACTAT 3426
                                         GCCACTGGCAGCCACTGGTAAC 3486
                                                                                 AGAGTTCTTGAAGTGGTGGCCTAAC 3546
                                                                                               obacteria; Pseudomonadales;
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/organism="Pseudomonas aeruginosa"
/mol type="genomic DNA"
/mol type="genomic DNA"
/fatain="MSH"
/db xref="taxon:287"
/clone="msh"
/clone="msh"
/note="Environmental isolate. Whole genomic
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Pred. No. 1.9e-197;
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 844)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Braceriol., (2002) In press
Contact: Chris K. Raymond
Cantact: Chris K. Raymond
Cantact: Chris K. Raymond
Cantact: Chris K. Raymond
Cantact: Chris K. Sauttle, WA 98105-2145, USA
Tel: 2062816954
Fax: 2066857244
Email: craymond@u.washington.edu
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914 bp DNA linear GSS 17-DEC-2002 pacs2-164_8370.x1 pacs2-164_B8370, genomic survey sequence.
BZ569398
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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/db xref="taxon:287"
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/clone=lpacs2-164"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library.
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Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, E.E., Hastings
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
12 2066857244
Eax: 2066857244
Email: craymond@u.washington.edu
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Location/Qualifiers
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Contact: Chris K. Raymond
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msh2_2771.x1 msh Pseudomonas aeruginosa genomic clone msh2_2771, pseudomonas aeruginosa genomic clone msh2_27711, pseudomonas aeruginosa genomic clone msh2_27711,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2895 ATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTC 2954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCTTTCGGGAAGCGTGGCGCTTTC 563
                                                                                                                                                                                                                                                                                                                                                      Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                      Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAATCGGCCAACGCGGGGGGGGGGGTTTGCGTATTGGCGCTCTTCCTC
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Pred. No. 3e-196;
0; Mismatches 110; Indels 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
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    1346
    /organism="Pseudomonas /mol_type="genomic DNA" strain="MSH"

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1 (bases 1 to 1346)
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clone="msh2_2771"
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Best Local Similarity 87.9%;
Matches 855; Conservative
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AUTHORS
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14.0%; Score 740.8; Distry 98.7%; Pred. No. 5.8e.3 TCGGCTTCCTGGCTCACTGACTGGCTGCGGGGGTTATCGGTTCCTGGCTGCTGACTGGTTATCGGTTATTTTATGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATTTTATGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATCGGTTATTTTATGGTTATCG		DB 29; Length 914; e-196; i 9; Indels 1; Gaps 1;	CICGGICGITCGGCTGCGGCGAGCG 2997	credercerredecrededededa 169	CACAGAATCAGGGGATAACGCAGGA 3057	CACAGAATCAGGGATAACGCAGGA 229	SAACCGFAAAAAGGCCGCGTTGCTG 3117	BAACCGTAAAAAGGCCGCTTGCTG 289	ICACAAAATCGACGCTCAAGTCAG 3177	ICACAAAAATCGACGCTCAAGTCAG 349	3337	GGGTTTCCCCCTGGAAGCTCCCTC 409	ATACCTGTCCGCCTTTCTCCCTTCG 3297	ATACCTGTCCGCCTTTCTCCCTTCG 469	3TATCTCAGTTCGGTGTAGGTCGTT 3357		FCAGCCCGACCGCTGCGCCTTATCC 3417	rcagcccgaccgccrrarcc 589	GAACTTATGGCGACTGGCAGCG 3477	GACTTATCGCCACTGCAGCC 649	CGGTGCTACAGAGTTCTTGAAGTGG 3537	CGGTGCTACAGAGTTCTTGAAGTGG 709	IGGTATCTGCTCTGCTGAAGCCA 3597	IGGTATCTGCGCTCTGCAGCCA 769	CGGCAAACAACCACCGCTGGTAGC 3657	GGGAAAC-AACCACGGTGGTAGC 828	CAGAAAAAG 3703	
	 11	14.0%; Score 740.8; :y 98.7%; Pred. No. 5.8 ervative 0; Mismatches	TCCGCTTCCTCGCTCACTGACTCGCTGCGCT	rccecricacicacidadricacidedr	GCTCACTCAAAGGCGGTAATACGGTTATCCA	GCTCACTCAAAGGCGGTAATACGGTTATCCA	ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA		TTCCATAGGCTCCGCCCCCTGACGAGCATC	TTCCATAGGCTCCGCCCCTGACGAGCATC	CGAAACCCCGACAGGACTATAAAGATACCAGG	CGAAACCCGACAGGACTATAAAGATACCAGG	TCTCCTGTTCCGACCCTGCCGCTTACCGGAT	TCTCCTGTTCCGACCTGCCGCTTACCGGAT	GTGGCGCTTTCTCATAGCTCACGCTGTAGGT	GTGGCGCTTTCTCATAGCTCACGCTGTAGGT	AAGCTGGGCTGTGCACGAACCCCCGTTC	AAGCTGGGCTGTGTGCACGAACCCCCCGTTC	TATOGTCTTGAGTCCAACCCGGTAAGACACG	TATCGTCTTGAGTCCAACCCGGTAAGACACG	AACAGGATTAGCAGAGCGAGGTATGTAGGCG	AACAGGATTAGCAGAGCGAGGTATGTAGGCG	AACTACGGCTACACTAGAAGAACAGTATTTG		TTCGGAAAAGAGTTGGTAGCTCTTGATCCG	CTTCGNAAAGAGTTGGTAGCTCTTGATCCG	TTTTTTGTTTGCAAGCAGCAGAATTACGCGCA	GGTGGTTTTTTTTTTGCAGCAGCAGATTACGCGCAGAAAAGG

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February 15, 2004, 19:10:26; Search time 1979.02 Seconds (without alignments) 10335.846 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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AR028794 Sequence AR050544 Sequence AR050546 Sequence AR041121 Sequence AR241123 Sequence AR241123 Sequence BD131785 Transfect BD145112 Methods a E00836 Recombinant I49834 Sequence 2 I49836 Sequence 2

AR241123 BD131785 BD145110 BD145112

AR094363 AR241121

K03104 Human cytom AX282811 Sequence

A85308 Sequence 6 BD107647 FIV vacci A92081 Sequence 5

A85308 BD107647

149836 HS5IEE AX282811

AR230688

A92080 Sequence 4 AR230690 Sequence A92077 Sequence 1 AR230692 Sequence

AR230690 A92077

AR230692

BD136066 Novel pro
BD136064 Novel pro
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BD136064 Novel pro
BD36064 Novel pro
BD36064 Sequence
AXS36741 Sequence
AXS91955 Sequence
AXS91955 Sequence
BD600145 Vector ha
10530 Sequence 16
108105 Sequence 3
M64941 Human cytom
M64940 Human cytom
M64940 Human cytom BD000143 Vector ha 105393 Sequence 14 108103 Sequence 1 A10617 Human Cytom AR028792 Sequence Rous sarc K02374 Rous-assoc Rous-assoc score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES 108105 HSSPIE1AB HSSPIE1AE HSSPIE1AF HSSPIE1AC AF052428 ALELTR2 AX256412 AX591955 BD000145 A10617 AR028792 AR028794 ALEENV DB Length Query Score Result No.

ALIGNMENTS

VRL 28-APR-1993 Rous-associated virus type 2
Louses; Retroid viruses; Retroviridae; Alpharetrovirus.

| (bases 1 to 1560)
| Rizub, D., Katz, R.A. and Skalka, A.M.
| Nucleotide sequence of noncoding regions in Rous-associated virus-2: comparisons delineate conserved regions important in replication and oncogenesis linear ALEENV 1560 bp se-RNA Rous-associated virus-2 env and gag genes. GI:210069 K02374.1 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE RESULT 1 ALEENV LOCUS

is the number of results predicted by chance to have a

Pred. No.

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Direct Submission
Submitted (04-MAR-1998) Fox Chase Cancer Center, 7701 Burholme Ave,
Philadelphia, PA 19111, USA
Location/Qualifiers
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PGNNPFFDNASNSKPFTVVTADRHNLFMGSEYCGAYGYRFWEMYNCSQWRQNWSICQ
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ADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAAPST
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EDWPTDWPVVTYTALDGGGIPWRKSRDMILIITISE
EDWPTDWPVVTANPQIHGIGGGIPWRKSRDMILLDFAVAMVR
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JLLVVCLPCLLQIVCGNIRKMINNSISYHTEYKKLQKAYGQPESRIV"
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AEVEALMSSPLLPHDVTNIMRVILGPAPYALMMDAWGVQLQTVIAAATRDPRHPANGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="envelope glycopolyprotein"
protein id="AAC08989.1"
db_xref="G1:3003003"
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| gene="env"
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1836. .2129
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/product="p12"
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/note="R"
22. .101
/note="U5"
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                                                                                                                                                                                                                                                                                          /protein id="AAA42546.1"
/boctein id="AAA42546.1"
/cranslate.non="NITTSLGDLDDVTSIRHAVLQNRAAIDFLLLAHGHGCEDIAG
MCCFNLSDHSESIQKKFQLMKEHVNKIGVNNDPIGSWLRGLFGGIGBWAVHLLKGLLL
GLVVILLLVVCLPCLLQCVSSIRRMIDNSLGYREFYKKITGGL
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1420. .>1560
Inde="aag polyprotein"
Codon_grart=1
protein_id="MAAA42547.1"

db_xref="GI:210071"

Lranslation="MEAVIKVISSACKTYCGKTSPSKKEIGAMLSLLQKEGLITSPSD
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J. Virol. 49 (2), 557-565 (1984)
84115081
6319755
Original source text: Rous-associated virus-2 covalently closed circular DNA, clone lambda-RAV2-2.
Location/Qualifiers
1. .1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF052428 9396 bp DNA linear VRL 01..
Rous sarcoma virus strain Schmidt-Ruppin B, complete genome
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Bouck, J., Salka, A.M. and Katz, R.A.
Complete nucleotide sequence of avian sarcoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.4%; Score 182; DB 14; Length 1560; Best Local Similarity 99.6%; Pred. No. 2.7e-99; Matches 232; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="c in one clone; t in another clone" 099
                                                                                                                                           /organism="Rous-associated virus type 2"
/mol_type="genomic RNA"
/db_xref="taxon:11948"
/db_i..441
/note="env polyprotein"
/codon_start=1
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2 (bases 1 to 9396)
Bouck,J., Skalka,A.M. and Katz,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      022. .>1560
product="viral mRNA"
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bp upstream of SphI site.
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AF052428.1 GI:3003000
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note="LTR'
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Rous sarcoma virus
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cleavage site; endonuclease cleavage site; long terminal repeat (LTR); reverse transcriptase endonuclease cleavage site.

Rous-associated virus type 2
Rous-associated virus type 2
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

Ubases 1 to 346)

Duyk,G., Leis,J., Longiaru,M. and Skalka,A.M.
Selective clavage in the avian retroviral long terminal repeat sequence by the endonuclease associated with the alpha beta form of avian reverse transcriptase
                                                                                                  ALELTR2
Rous-associated virus 2 (RAV-2) LTR with reverse transcriptase endonuclease cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Original source text: Rous-associated virus 2 replication form I DNA, clone RAV2-2 [1], and plasmids pFG1 and pGJ4 [2].

Reverse transcriptase associated endonuclease (purified from avian sarcoma virus) cleavage sites have been mapped in two tandemly linked Rous-associated virus-2 LTR sequences. The enzyme may be involved in viral cDNA integration in the host, since it generates a 6 bp staggered overlap that spans the junction. The clone sequence (RAV2-2) corresponds to the unintegrated replicative form [RR) I of RAV-2.

Location/Qualifiers
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Skalka,A.M., Duyk,G., Longiaru,M., DeHaseth,P., Terry,R. and
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/note="rt-endonuclease secondary cleavage site"
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Cold Spring Harb. Symp. Quant. Biol. 49, 651-659 (1984)
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84070706
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    346
    organism="Rous-associated virus type 2"

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/note="rt-endonuclease secondary
complement (244. .245)
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/db_xref="taxon:11948"
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/note="rt-endonuclease
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/note="ltr B"
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RGLGPLQI WOTDFTLEPRMARRSMILAVTVDTASSAIVTOGHGKVTGVYAGGHHWATAIA
VLGP FKAIKTDNGSCFTSKSTREMLARWGIAHTTGIPGNGSGGQAMVERANRLLKDKIR
VLABGDGFRKKRIPASKÇGELLAKAMYALNHFERGEMTKTPVQKHWRPTVLTEGEPPVKI
RIETGEWEKGWNVLVWGRGYAAVKNRDĪDKVIWVPSRKVKPDITQKDEVTKKDEASPL
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RTPSRSFGTVATEPKLFGDFNTSDTVTSPQRAGALAGGVTFVALXDYBEWIETDLSF
RTPSRSFGTVATEPKLFGDFNTSDTVTSPQRAGALAGGVTFVALXDYBEWIETDLSF
KLLANPENDRGTFLWRSETTKGAYCLSVSPPDNAKGLNVKHYKIRKLDSGGFYTTSR
QFSSLQQLVAYYSKHADGLCHRLTNVCPTSKPQTGGLAKDAWEIPRESLRLEVKLGGG
CFGEWWMGTWNGTTRVGTWNGTTRVAIKTLKFGTMSPEAFLQBAQVMKKLRHEKLVQU
YAVVSEEPIYIVIEYMSKALDFGLARLEDMSTYARLOGAKFPIKATABGAAYVERMYY
HRDLRAANILVGENIVYCKVADFGLARLEDMSTYARQGAKFPIKWTAPABAAAVGRRYYY
KSDVMSFGILLITELTTKGRMPYPGMGNGSVLDRVERGYRMFCPPECPBSLHDLMCQCW
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                                                                                                                                                                                               codon_start=1
product="polymerase and integrase protein"
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protein_id="AAC08990.1"
db_xref="G1:3003004"
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lb_xref="GI:3003002"
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/rpt_type=direct
9131. .>9396
9131. .9375
/note="U3"
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/rpt_type=direct
7300. .8908
/gene="src"
                          /gene="gag"
/product="p15".
<2522. .5210
/gene="p01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300. .8907
|gene="src"
|codon_start=1
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9376. .>9396
/note="R"
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gene="pol"
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16-JAN-1998 US 60/071673

DONNA ARMENTANO, NELSON YEW, JOHN MARSHALL

C12N15/09, AGIX55/76, AGIX49/00, C12N15/00

Novel promocer element for sustained gene expression FH

Location/Qualifiers
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C12N15/09, A61X35/76, A61X48/00, C12N15/00
Novel promoter element for sustained gene expression
Location/Qualifiers
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BD136064
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Cytomegalovirus
Cytomegalovirus
Cytomegalovirus
Viruses, dsDNA yruses, no RNA stage, Herpesviridae,
1 (bases 1 to 512)
Armentano,D., Yew,N. and Marshall,J.
Novel promoter element for sustained gene expression
GENZIME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 127; DB 6; Length 282; larity 100.0%; Pred. No. 1.4e-65; Conservative 0; Mismatches 0; Indels
         no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                     organism='Cytomegalovirus'
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Location/Qualifiers
                                1 (bases 1 to 282)
Armentano, D., Yew, N. and Marshall, J.
Novel promoter element for sustained gene
Patent: JP 2002508974-A 2 26-MAR-2002;
GENZYME CORP
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/organisme="Cytomegalovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10358"
1 65 c 72 g 77 t

    .512
    /organism="Cytomegalovirus"

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JP 2002508974-A/1
26-MAR-2002
15-JAN-1999 UP 2000540258
16-JAN-1998 US 60/071673
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     Viruses; dsDNA viruses,
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JP 2002508974-A/1.
                                                                                                                        Cytomegalovirus
JP 2002508974-A/2
26-MAR-2002
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Best Local Similarity
Matches 127; Conserv
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BD136064
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207 TGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGGAG 266
                                                                              267 TAAGGTGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAGGGAACAGACGGGTTAAAC 326
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                                                   319 TAAGGTGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAGGCAACAGACGGGTCTAAC 378
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16-JAN-1998 US 60/071673
DONNA ARRENTANO, NELSON YEW, JOHN MARSHALL
C12N15/09, A61X55/76, A61X48/00, C12N15/00
Novel promocer element for sustained gene expression FH
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Novel promoter element for sustained gene expression.
BD136066
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Location/Qualifiers
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Armentano, D., Yew, N. and Marshall, J.
Novel promoter element for sustained g
Patent: JP 2002508974-A 3 26-MAR-2002;
GENZIME CORP
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/organism="Cytomegalovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10358"
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                                                                                                                                           327 ACGGATTGGACGAACCACTG 346
                                                                                                                     379 ACGGATTGGACGAACCACTG 398
                                                                                                                                                                                                                                                                                                                                             Cytomegalovirus
Viruses; dsDNA viruses,
Betaherpesvirinae.
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JP 2002508974-A/3.
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JP 2002508974-A/2.
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JP 2002508974-A/3
26-MAR-2002
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Best Local Similarity 100.0
Matches 127; Conservative
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Cytomegalovirus
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BD136066
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| cauliflower mosaic virus promoter', ...590 | crossing the continuent of contin
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                                                                                                                                                                                                          TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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C12N15/09, C07K14/61, C12N1/13, C12P21/02, C12N15/00 CC
Key
                                                                                                     Length 512;
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                   tch 25.4%; Score 127; DB 6; L al Similarity 100.0%; Pred. No. 1.4e-65; 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 590)
Hawkins, R. and Nakamura, M.
Signal peptide
Patent: JP 200054490-A 3 26-DEC-2000;
TOYOTA MOTOR CORP
                                        132 t
/mol_type="genomic DNA"
/db_xref="taxon:10358"
131 c 123 g 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 bp
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JP 2000354490-A/3.
unidentified
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E59416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
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                                                                                                   Query Match
                                                                                                                        Best Local
Matches 12
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DEFINITION
ACCESSION
VERSION
SOURCE
ORGANISM
                                      BASE COUNT
ORIGIN
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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E59416
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ES1990 Stombinant containing the same and utilization thereof. ES1990
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C12N15/09, A61K31/00, A61K31/00, A61K39/02, A61K39/17, A61K39/215,
C07K14/125,
C07K14/165, C07K14/30, C12N1/00, C12N15/00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
                                                                                                                                                                                                                                                                                          same and utilization thereof
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
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0
                                                                                 E51990.1 GI:18629551

E51990.1 GI:18629551

Human herpesvirus 5

Human herpesvirus 5

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.

I (Dases 1 to 599)

Kubomura,M. and Saito,S.

Promocer, recombinant containing the same and utilizati
Patent: JP 201000188-A 5 09-JAN-2001;
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
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/organism="Human herpesvirus 5"
/mol_type="genomic DNA"
/db_xref="taxon:10359"
114 c 144 g 159 t
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CORIXA CORPORATION (US)
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Seguence 425 from Patent WO0202623.
AX360741
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JP 2001000188-A/5
09-JAN-2001
22-JUN-1999 JP 1999174804
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1. .600
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Vector having stabilized sequence and eucaryotic host cell. BD000145 BD000145 BD000145 BD0000145 BD0000145 BD0000145. Unidentified midentified
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/ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Patent: JP 2000308497-A 3 07-NOV-2000;
GENETIC INC
OS Unidentified
PN JP 2000308497-A/3
PD 07-NOV-2000
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Location/Qualifiers
                              Lin, J., Yaver, D., Foster, D. and Holly, R.
Methods for expressing endogenous genes by re
mediated integration
Patent: WO 0236760-A 24 10-MAY-2002;
Novozymes Biotech, Inc. (US); ZymoGenetics,
Location/Qualifiers
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1. .773
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/mol_type="genomic DNA"
/db_xref="temport"
a _205 c 190 g 194
                                                                                                                                                   /organism="Mus musculus"
/mol type="genomic DNA"
/db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unclassified.
1 (bases 1 to 777)
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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ORIGIN
                                    AUTHORS
TITLE
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BD000145
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TITLE
JOURNAL
                    REFERENCE
                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 TITIGGCAGTACAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGGCTT 373
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                                                                                                                                                                                                                                                                        338 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 397
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GACTITICTACTIGGCAGIACAICIACGIAITAGICAICGCIAITACCAIGGIGAIGCG
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ROHM AND HAAS COMPANY (US)
Location/Qualifiers
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                                                                                                                                     0; Indels
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                                                                                                  Ouery Match 25.4%; Score 127; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 127; DB 6; I
Pred. No. 1.4e-65;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
a 164 c 155 g 150 t
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Sequence 24 from Patent W00236760.
AX591955
AX591955.1 GI:27950185
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Sequence 60 from Patent W00170816.
AX256412
AX256412.1 GI:16075237
 organism="Homo sapiens"
                /mol_type="genomic_DNA"
/db_xref="taxon:9606"
152 c 141 g 15
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synthetic construct
artificial sequences.
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Matches 127; Conservative
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AX591955
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AX256412
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VRL 02-AUG-1993

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343 GACTITCCTACTIGGCAGIACATCTACGIAITAGTCATGGCTATTACCATGGTGATGCGG 402
                                                                            403 TITITGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 462
                                                   TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 875)
Lehner,R., Stamminger,T. and Mach,M.
Comparative sequence analysis of human cytomegalovirus strains
J. Clin. Microbiol. 29 (11), 2494-2502 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Human herpesvirus 5"
/mol_type="genomic DNA"
/db_xref="taxon:10359"
/cell_line="infected human foreskin fibroblast"
209 c 201 g 238 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 875;
                                                                                                                                                                                                                                                                                    M64941.1 GI:330635
enhancer region; promoter region.
Human herpesvirus 5
Human repesvirus 5
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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Human cytomegalovirus IE-1 promoter region.
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
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                                       TITITGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGAATTTCCAAGTCTC 462
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Gorman.C.M.
A transient expression system for producing recombinant protein
Patent: EP 0309237-Al 3 29-MAR-1989;
10-0ation/Qualifiers
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25.4%; Score 127; DB 6; Length 777;
Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
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Location/Qualifiers
                                                                                                                                                                                             Sequence 16 from Patent EP 0260148.
105430
105430.1 GI:591075
                TTTTGGCAGTACATCAATGGGCGTGGATAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
188 a 205 c 190 g
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205 c 190 g
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Unclassified.
1. (bases 1 to 777)
Gorman, C.M.
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Cytomegalovirus de Partial expression DNA sequence of po CMV enhancer/Myelo

CMV promoter

DNA sequence of po Enhancer for eukar HCMV (AD169) major Sequence of HCMV(A HCMV immediate ear Adeno-associated v

AAL4414 AAZ55643 AAN82490697 AAD53783 AAD81527 AAN80595 AAN60156 AAC53550 AAC53550 AAC53550 AAC55629 AAC5629 AAC5629

10 10 25

Partial expression

Run

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Human, vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1; chronic limb ischaemia; myocardial ischaemia, autoimmune disorder; pHE4a; allergic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferative disorder; viral infection; bacterial infection; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; embolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector construct pVGI.1 containing VEGF-2 insert.
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Synthetic.
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Cytomegalovirus-de
S2 subtraction lib
Cytomegalovirus (C
Human cytomegalovi
Cauliflower mosaic
Cytomegalovirus (C
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                                                                                               February 15, 2004, 19:07:11; Search time 161.871 Seconds (without alignments) 8338.264 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                | S1DS1/gcgdata/genseqq.gensegqn.emb1/NA1981.DAT:*
| S1DS1/gcgdata/genseqq.gensegqn.emb1/NA1981.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1981.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1981.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1984.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1984.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1985.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1985.DAT:*
| S1DS1/gcgdata/genseqq.emb1/NA1987.DAT:*
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| S1DS1/gcgdata/genseqq.emb1/NA1987.DAT:*
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SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:
SIDSI/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
/SIDSI/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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AAH24425
AAF84456
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AAX80727
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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DNA encoding CTLA-CMV-PC-PSA promote CMV-PSA promoter. DNA encoding Synec CMV promoter / mou Chimeric sequence Chimeric sequence Wild-type human Ap

ABX04557 AAL44408

1467

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Human ovarian anti Transgenic APP DNA

DNA encoding N-ter Promoter-enhancer CMVintA promoter a

ABX04567 AAN91042

ALIGNMENTS

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Reporter gene cons

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AAH28445 AAV58058

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Cytomegalovirus-derived promoter element-2 (-299
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                                                                                                                                expression vector construct containing the vacular endothelial growth factor 2 (VBGF-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell with the DNA and for treating a parient having chronic limb ischaemia or myocardial ischaemia, or a disease or disorder selected from autoimmune disorders (e.g. rheumatoria arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease), diseases due to viral, bacterial, fungal or parasitic infection, cardiovascular disorders (e.g. cardiowascular disorders (e.g. cardiowascular disorders and embolism. This sequence represents the pVGI.1 expression vector containing the VBGF-2
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                          Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischaemia or myocardial ischaemia, autoimmune disorders and allergic
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                                                                                                                     The invention relates to an isolated nucleic acid comprising pVGI.1
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                                                                                                                                                                                                                                                                                                                                                         Length 5283;
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100.0%; Pred. No. 4.1e-262;
tive 0; Mismatches 0;
                                                                                             Disclosure, Fig 31; 241pp; English.
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WPI; 2002-217153/27
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nes 500;
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AAX80727 standard; DNA; 281

AAX80727

RESULT 2
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The present sequence is a promoter element derived from the cytomegalovirus (CWV) immediate early promoter. The promoter the promoter element is used to achieve persistent expression of an operably linked transgene, especially human cystic fibrosis transmembrane conductance regulator especially human cystic fibrosis transmembrane conductance regulator expression of human alpha-galactostidase gene, in a target cell. The expression cassette comprising the promoter element operably linked to a transgene is delivered to a target cell via a plasmid or an adenoviral vector lacking the B4 region. As the promoter element functions independently of the viral genomes thereby increasing the carrying capacity containing reduced viral genomes thereby increasing the carrying capacity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing reduced viral genomes thereby increasing the carrying capacity of the vector while decreasing the potential for host immune reaction.
Cytomegalovirus-derived promoter element-2; CMV-derived promoter element; cytomegalovirus immediate early promoter; human alpha-galactosidase gene; persistent transgene expression; expression cassette; human CFTR gene; human cystic fibrosis transmembrane conductance regulator gene; adenoviral vector; E4 region; transgene; plasmid; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytomegalovirus (CMV)-derived promoter element and human albumin one enhancer elements useful for persistent gene expression
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CMV_derived_promoter_element
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Matches 127; Conservative
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                                                                                                                                                                                     Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Armentano D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-1998;
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ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and ABP54446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 434
                                                                                               Human, cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
immune response; virology; immunology; microbiology; molecular biology;
recombinant DNA technology; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic polynuclectides or polypeptides useful for diagnosing preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GACTITICCTACTIGGCAGIACATCTACGIATTAGTCATCGCTATTACCATGGTGATGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.4%; Score 127; DB 25; Length 481; Best Local Similarity 100.0%; Pred. No. 8e-59; Matches 127; Conservative 0; Mismatches 0; Indels C
                                                     $2 subtraction library cancer related clone SEQ ID NO:412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 481 BP; 121 A; 119 C; 109 G; 132 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaiger A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 412; 207pp; English.
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28-AUG-2001; 2001US-315563P.
09-JAN-2002; 2002US-347313P.
                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002WO-US10421.
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recombinant DNA techniques
       (first entry)
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                                                                                     Cytomegalovirus-derived promoter element-1; CMV-derived promoter element; cytomegalovirus immediate early promoter; human alpha-galactosidase gene; persistent transgene expression; expression cassette; human CFTR gene; human cystic fibrosis transmembrane conductance regulator gene; adenoviral vector; E4 region; transgene; plasmid; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GACTITCCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GACTITICITACITIGGCAGTACATCITACGIATTAGTCATCGCTATTACCATGGTGATGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A cytomegalovirus (CMV)-derived promoter element and human albumin gene enhancer elements useful for persistent gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.4%; Score 127; DB 20; Length 282; 100.0%; Pred. No. 8.1e-59;
                                              Cytomegalovirus-derived promoter element-1 (-295 to -14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                1..282
/*tag= a
/label= CMV_derived_promoter_element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 282 BP; 68 A; 65 C; 72 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Pages 48-49; 56pp; English.
                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yew N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABZ17986 standard; cDNA; 481 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US00915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0071673
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marshall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCCCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-478911/40.
                                                                                                                                                                                                                                 Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Armentano D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                           WO9936557-A1
  19-0CT-1999
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                                                                                                                                                                                                                                                                                                     promoter
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AC ABZ1

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Gaps

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Score 127; DB 19; Pred. No. 8e-59;); Mismatches 0;

Length 500; Indels 136 350

290

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growth

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apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis; Human cytomegalovirus promoter region; ss.
 administered to a patient having a disease associated with an aberrant
                                                                                                                                                                              231 GACTITCCIACITGGGAGIACAICTACGIAITAGICAICGCIAITACCAIGGGGAGGGG
                                                                                                                                                                                                                                                                291 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                              77 ITTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGGATTTCCAAGTCTC
                                                                                                                                                         17 GACTITICCTACTIGGCAGIACAICIACGIAITAGICAICGCTAITACCAIGGIGAIGCGG
                                                    Seguence 500 BP; 121 A; 126 C; 125 G; 128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus promoter region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guevara JG, Hoogeveen RC, Moore JP;
                                                                          25.4%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                           5163/c
AAX15163 standard; DNA; 589 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0079030
97US-0874807
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                                                                                                                       Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                   351 CACCCCA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070331/06.
                                                                                                        Similarity
                    form of the gene.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA containing inactive, mutated binding site for Gfi-1 transcription repressor - used to increase gene expression in vitro
                                     transcription repressor; mutation; cytokine; gene therapy; factor independence-1; cytomegalovirus; promoter; ss.
Cytomegalovirus (CMV)-MIE wild-type promoter sequence.
                                                                                                                                                                                                                                                                                                                                                    88.399
*tag= e
note= "putative Gfi-1 binding site"
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note= "putative Gfi-1 binding site"
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"G can be substituted by
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"C can be substituted by
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                                                                                                                     Location/Qualifiers
331..342
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anscription repressor - used to
in vivo, e.g. in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FOXC-) FOX CHASE CANCER CENT.
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                                                                                       Human cytomegalovirus
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                                                                                                                                          misc binding
                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                      misc_binding
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Grimes HL,

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The present sequence represents the Human cytomegalovirus promoter region. The compositions of the invention bind to this sequence. The specification describes a composition that comprises low density lipoprotein (LDL) and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or riboxyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and
Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 589 BP; 157 A; 140 C; 143 G; 149 T; 0 other;
                                                                                                                                                                                                                                     Example 4; Page 74; 293pp; English.
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The invention relates to a 5' and a 3' fragment of the chicken beta-actin promoter (AAP84452 and AAP84453, respectively), which exhibit promoter activity. The chicken beta-actin promoter fragments may be used to drive expression of a heterologous gene in a recombinant vector used as the active component of a genetic vaccine. The present sequence represents a cyclomegalovinus (GWN) immediate-early (IR) promoter aniancer, a portion of which was used in the construction of the chimeric Pec promoter (AAF84454) in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                  374 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGITIGACICACGGGGAITICCAAGICIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant
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0
                                                                                                                                                                                                                                                            Cytomegalovirus (CMV) immediate-early (IE) promoter enhancer
                                                                                                                                                                                                                                                                                        Cytomegalovirus; CMV; immediate-early; IE promoter enhancer; Pec promoter; chicken beta-actin promoter; recombinant vector; genetic vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.4%; Score 127; DB 22; Length 599; 100.0%; Pred. No. 8e-59; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule for use as a promoter for preparing a recontaining the DNA which is used for preparing a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 599 BP; 152 A; 144 C; 144 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 12; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK16313 standard; cDNA; 600 BP.
                                                                                                                                                                AAF84456 standard; DNA; 599 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0174804.
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                                                                                                                                                                                                                                                                                                                                                           Human cytomegalovirus
                                                                                 440
                                                   CACCCCA 143
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JAPG ) NIPPON ZEON
                                                                                 CACCCCA
                                                                                                                                                                                                                                                                                                                                                                                          JP2001000188-A.
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                                                                                                                                                                                                                             25-JUN-2001
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                                                 137
                                                                                                                                                                                              AAF84456;
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                                                                                 434
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ID ABKI
                                                                                                                                 RESULT 8
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                                                                                                                          77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                             276 GACTITICCTACTIGGCAGIACATCTACGIATTAGTCATCGCTATTACCATGGTGATGCGG 217
                                                                                                                                                GACTITICCTACTIGGCAGIACAICTACGIATIAGICAICGCIAITACCAIGGIGAIGCGG 373
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X 2 = Gly-Ser-Leu or Pro-Leu-Ala,
The signal peptides are useful in the preparation of human growth
hormone and transformed chlorella. Signal peptides, DNA encoding the
hopptides, gene expression cassettes, recombinant vectors containing the
cassettes, and transformants having the vectors are provided. The
present sequence is a promoter which may be used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is provided in a specification relating to signal peptides for expression and secretion of a protein in chlorella. The peptides are of the formula Met-Ala-Asn-Lys-X_1-(Leu)_n-X_2-Ala-Ser-Gly.
X_1 = Ser or Leu;
n = an inferent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal peptides useful for the preparation of human growth hormone transformed chlorella
                                                                17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                   Gaps
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0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cauliflower mosaic virus; promoter; signal peptide; chlorella; gene expression; protein production; human growth hormone; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.4%; Score 127; DB 22; Length 590; Best Local Similarity 100.0%; Pred. No. 8e-59; Matches 127; Conservative 0; Mismatches 0; Indels (
 Score 127; DB 20; Length 589;
Pred. No. 8e-59;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 590 BP; 149 A; 143 C; 141 G; 157 T; 0 other;
                                   ò
25.4%; Score 127; DB
ilarity 100.0%; Pred. No. 8e-
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Cauliflower mosaic virus promoter,
                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                           590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0168271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0168271,
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                         AAH24425 standard; DNA;
                                                                                                                                                                                             CACCCCA 143
                                                                                                                                                                                                                           CACCCCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-275809/29.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP2000354490-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000.
                                  127;
                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                        AAH24425;
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                    Best Loca
Matches
                                                                                                                                                                                                                                                                                            AAH24425
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gene expression systems useful for modulating gene expression in host cells. The gene expression system encodes a polypeptide with a DNA-binding domain recognizes a response element associated with a Good whose expression is to be modulated and/or a ligand binding domain (IBD) comprising a LBD from a nuclear receptor and a second gene expression cassette capable of being expressed in a host cell comprising a transpolymucleotide sequence encoding second polypeptide comprising a transpolymucleotide sequence encoding second polypeptide comprising a transpolymucleation domain and/or a LBD comprising a LBD from a nuclear receptor other than an ecdysone receptor, a retinoid X receptor or a USP receptor and the LBDs from the first and second polypeptides are different and dimerise). The ecdysone and retinoid X receptor based inducible gene expression systems useful for modulating gene expression inducible gene expression systems useful for modulating gene expression proteins and antibodies, cell-based high-throughput screening assays (HTS), functional genomic and regulation of traits in transgenic plants and animals. The present sequence represents a cauliflower mosiac virus, CWV, promoter which is used in an inducible gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Ecdysone and retinoid X receptor based inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGIIITGACICACGGGGAITIICCAAGICIC
                          transactivation domain, nuclear receptor, ultraspiracle, gene thera
protein production, antibody production, high throughput screening,
                                                                                                                                                                                                                                                                                                                                                                                                                        Ecdysone and retinoid X receptor based inducible gene expression systems for use in e.g. gene therapy, large scale production of
      CMV promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 127; DB 22; Length 619;
Pred. No. 8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                            systems for use in e.g. gene therapy, large scale product proteins and cell-based high-throughput screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 619 BP; 150 A; 164 C; 155 G; 150 T; 0 other;
        retinoid X receptor; RXRalpha; DNA-binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                            HTS; transgenic plant; transgenic animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 140-141; 144pp; English
                                                                                                                                                                                                                                                                                                                                                Cress DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL44414 standard; DNA; 738 BP.
                                                                                                                                                                                                               21-MAR-2001; 2001WO-US09050
                                                                                                                                                                                                                                                   22-MAR-2000; 2000US-191355P.
20-FEB-2001; 2001US-269799P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.4%;
                                                                                                                                                                                                                                                                                                                                                Kapitskaya MZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Lov.
Matches 127; Conservative
                                                                                                Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                          (ROHM ) ROHM & HAAS CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656841/75.
                                                                                                                                    WO200170816-A2
                                                                                                                                                                           27-SEP-2001,
                                                                                                                                                                                                                                                                                                                                              Palli SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL44414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
AAL44414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides. Compositions comprising the lung tumour polypeptides, polypeptides, fusion proteins, antibodies to the polypeptides, T cell populations, or antigen presenting cells that express the lung tumour polypeptides, are useful for treating lung cancer or stimulating an immune response. The polymucleotides and polypeptides are also useful in the diagnosis and monitoring of lung cancer. Sequences ABK15889-AAS16343 represent CDNA molecules encoding the polypeptides of the invention and PCR primers used to amplify the CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTITICCTACTIGGCAGIACAICIACGIAITAGICAICGCIAITACCAIGGIGAIGCGG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGIIIGACICACGGGGAITICCAAGICIC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 397
                                                                                                              Human; lung tumour protein; lung cancer; immunostimulant; cytostatic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymucleotides encoding lung tumour polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTITCCTACTIGGCAGIACATCTACGIATTAGICATCGCIAITACCATGGIGAIGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides encoding lung tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henderson RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 25.4%; Score 127; DB 24; Length 600; al Similarity 100.0%; Pred. No. 8e-59; 127; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 600 BP; 153 A; 152 C; 141 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecdysone receptor; EcR; ligand binding domain; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter D,
                                                                        Human lung tumour protein encoding cDNA #425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 261-262; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wantanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mosiac virus promoter,
                                                                                                                                                                                                                                                                                                                    29-JUN-2000; 2000US-215696P.
22-AUG-2000; 2000US-227142P.
06-SEP-2000; 2000US-230481P.
21-DEC-2000; 2000US-257729P.
                                                                                                                                                                                                                                                                                 28-JUN-2001; 2001WO-US20975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS15664 standard; DNA; 619
                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcneill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-106602/14.
                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCCCA
                                                                                                                                                                                                         WO200202623-A2.
                                                                                                                                                                       Homo sapiens.
                                      14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2002
                                                                                                                                                                                                                                               10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cauliflower
                                                                                                                                primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS15664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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AAS15664
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08-JUN-2000

31-OCT-2002

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The method involves introducing a restriction enzyme and a nucleic acid regulatory sequence into mammalian cells - for integrating the nucleic acid construct into the mammalian cell genome at sites generated by the restriction enzyme. Mutant mammalian cells having a trait of interest can then be selected. The method of the invention is useful for isolating a gene controlling a trait of interest from a mammalian cell. The method is useful for discovering and isolating new genes. The method of the invention can be used to create large libraries of mammalian cells which have a low transfection efficiency. The method of the invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 gacitirectactificacagracarcracgrafragicardectarraccardergardegg 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 irriredekaracarcaaredeceredaradederrireacreacededarrireaagrere 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising a Cytomegalovirus (CMV) promoter and a murine G-CSF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suitable for over-expressing a known endogenous gene that is expressed poorly. The present DNA sequence represents a chimeric gene sequence
                                                        CMV promoter / mouse G-CSF receptor (G-CSFR) gene 9 - chimeric sequenc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 TITITGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises a method for producing a mutant mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production of a mutant mammalian cell for isolating genes, comprising integrating a nucleic acid construct into the cell genome at sites generated by the restriction enzyme, and selecting cell with trait of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                       Mouse, murine, ds, gene of interest isolation; CMV; gene, promoter, novel gene discovery, novel gene isolation, large library production; G-CSF receptor; G-CSFR; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127; DB 24; Length 738;
Pred. No. 8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 738 BP; 188 A; 178 C; 168 G; 204 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%; Fred. No. 8e-
Matches 127; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holly R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Fig 14; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ95643 standard; DNA; 763 BP
                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVOZYMES BIOTECH INC (ZYMO ) ZYMOGENETICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.48;
                                                                                                                                                                                                                                                                                                              30-OCT-2001; 2001WO-US45045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin J, Yaver D, Foster D,
                                                                                                                                                                                                                                                                                                                                                     30-OCT-2000; 2000US-0702177
                                                                                                                                                                          Chimeric - Mus sp.
Chimeric - Cytomegalovirus.
                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-566503/60.
                                                                                                                                                                                                                                     WO200236760-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
                                                                                                                                                                                                                                                                          10-MAY-2002
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AAZ95643
ID AAZ95
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AC AAZ95
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A method has been developed of increasing prostanoid production in vivo comprising delivering and hyperexpressing a prostaglandin synthase gene in cells. The method can be used for gene therapy. The method is useful for the treatment of diseases such as pulmonary embolus, myocardial infarction and general lung disease (e.g. adult respiratory distress syndrome). Generally the present invention provides a plasmid comprising a cytomegalovirus (GWV) derived promoter sequence driving the coding region for ovinine prostaglandin G/H synthase (PGH). In order to increase translation augmenting sequence and a portion of the 3' untranslated region from the human growth hormone (HGH) gene. The present sequence region from the human growth hormone (HGH) gene. The present sequence regions the computation of the sequence and a portion of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGITIGACICACGGGGAITICCAAGICIC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 tringgcagracarcaargggcgregaraggggringacrcacgggarriccaagrcic 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 dactriccractrescastracarctaceratrastratescarscratescratesces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
for
                                                                                   ovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing prostanoid production in vivo comprising delivering hyperexpressing a prostaglandin synthase gene in cells, useful treating e.g. myocardial infarction and general lung disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%; Score 127; DB 21; Length 763; 100.0%; Pred. No. 8e-59; o. Indels ()
                                                                                Cytomegalovirus, CMV, promoter; human growth hormone; PGH; prostaglandin G/H synthase; plasmid; prostanoid; circular; cardiant; thrombolytic; antiinflammatory; gene therapy; pulmonary embolus; myocardial infarction; lung disease; adult respiratory distress syndrome; ds.
                                                Cytomegalovirus derived promoter sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 763 BP; 203 A; 174 C; 164 G; 222 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Conary JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 7-10; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Brigham K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN82445 standard; DNA; 777 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.48;
                                                                                                                                                                                                                                                                                                                                  91US-0746941.
                                                                                                                                                                                                                                                                                                95US-0459493
                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Canonico A,
                                                                                                                                                                                                                                                                                                                                                                                    (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                            Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCCCA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention
                                                                                                                                                                                                                                                                                                02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                    19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                    21-JUN-1993;
                                                                                                                                                                                                                             US6030638-A,
                                                                                                                                                                                                                                                               29-FEB-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                       Meyrick B,
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AAN82445
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DNA sequence of portion of plasmid pF8CSSS containing the cytomegalovirus enhancer and promoter and an engineered stabilising.
                                                                                                                                                                                                                          /*tag= b honte="stabilising sequence including the engineered splice donor and acceptor sequence"
                                                                                                                                                                                                  'note="cytomegalovirus enhancer, promoter and leader
                                                                                          Plasmid pF8CSSS; cytomegalovirus; SV40; enhancer; promoter; stabilising sequence; splice donor intron sequence; Ig region; splice acceptor sequence; human embryonic kidney cells (293);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transient expression system for recombinant proteins - comprising eukaryotic host cell transfected with vector encoding trans-activating protein and expression vector
                                                                                                                                                                                                                                                                                  'note="remaining leader"
                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /note="Begin RNA"
                                                                                                                                                                                                                                                                                                                                                                                                               87US-0101712.
                         (updated)
(first entry)
                                                                                                                                                                                                            733..736
                                                                                                                                                                                       /*tag=
                                                                                                                                        Cytomegalovirus; SV40
                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-095394/13.
                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1987;
                       25-MAR-2003
15-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                  29-MAR-1989
                                                                                                                                                                                                                                                                                                                                            EP309237-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gorman CM;
  AAN90697;
                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                                                                                               misc_RNA
                                                                                                                                                                 Key
  462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCGCTATTACCTTGGTGATGCGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 ITTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In the expression vectors of the invention, the promoter is specifically from the immediate early gene of human cytomegalovirus (CMV) or from simian virus (SV40). The stabilizing SQ contains 1 or 2 splice donor-intron-acceptor SQs, esp. from the specified CMV gene, or the intron is from CMV or the Ig variable region, while the splice-acceptor component corresponds to the Ig acceptor SQ. The vector may also include (upstream of the promoter) an enhancer, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                               Expression vector; promoter; heterologous protein; mammalian vector;
                                                                                                                                                                                                                                                                                                                                                                                                    Continuous expression of heterologous protein in eukaryotic cells - by transfecting with vector contg. stabilising sequence, promoter, structural gene, poly:adenylate sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 777 BP; 188 A; 205 C; 190 G; 194 T; 0 other;
                                                                                                                              a
"from pPMLCMV beginning t
enhancers and promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 127; DB 9;
100.0%; Pred. No. 8e-59;
ative 0; Mismatches 0
                         Partial expression vector pF8CSSS sequence.
                                                                                                                                                               612
/*tag= b
/note= "starts here"
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example, Fig 19, 48pp, English.
                                                                                                                                                                                                                                                                                 87US-0071674.
86US-0907185.
87US-0101712.
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06-MAR-1992 (first entry)
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                                                                                                                             /*tag=
/note=
                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       termination site
                                                                                 Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      also from SV40
                                                                                                                   misc_feature
                                                                                                                                                                                                                                                            11-SEP-1987;
                                                                                                                                                                                                                                                                                               12-SEP-1986;
25-SEP-1987;
                                                                                                                                                                                                                                                                                  09-JUL-1987;
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                                                                                                                                                                 mRNA
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Expression vector pF8CSSS contains the cytomegalovirus enhancer and promoter, an engineered stabilising sequence, the cDNA encoding factor VIII and the SV40 polyademylation site. The entire intron region including donor and acceptor sequences was deleted and replaced by an engineered stabilising sequence. pF8CSSS is used in a method for prodn. of a desired heterologous protein in a eukaryotic host cell. The method comprises: transfecting a encaryotic host cell with an expression vector having a sequence of as DNA comprising, an expression vector having a sequence of a do DNA comprising, an expression vector having a sequence of the desired protein, and a polyencoding the anino acid sequence of the desired protein, and a polyencoding the anino acid sequence of the desired protein, and a polyenching the method provides useful quantitities of a desired protein in a relatively short period of time without having to establish continuous prodn. The transient expression system optimises the interaction between specific vector components and certain trans-activating proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.4%; Score 127; DB 10;
100.0%; Pred. No. 8e-59;
iive 0; Mismatches 0;
Disclosure; ; 44 pp.; English.
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Best Local Similarity 100.
Matches 127; Conservative
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RESULT 14 AAN90697 ID AAN90697 standard; DNA; 777 BP. XX

CACCCCA 469

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343 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCGCTATTACCTATGCGTGATGCGG 402
                                                                          TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                             403 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZNPP) 2 or ZNNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammanian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                  CMV enhancer/Myeloproliferative sarcoma virus LTR promoter construct DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF9; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; autoimmune disease; systemic lupus erychematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; cytomegalovirus; CWV; chimeric; gene; ds.
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408..884
/*tag= b
/note= "Myeloproliferative sarcoma virus LTR promoter"
17 GACTITCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane activator and calcium modulator and cyclophilin
ligand-interactor (TACI)-immunoglobulin fusion protein, for treating
cancer or diabetes, comprises a TACI receptor group and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric - Cytomegalovirus.
Chimeric - Myeloproliferative sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Column 141; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..407
/*tag= a
/note= "CMV enhancer"
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                                                                                                                                                                                                                                                                                   AAD53783 standard; DNA; 884 BP.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                137 CACCCCA 143
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AAD53783
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316 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGATTTCCAAGTCTC 375
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                                                                                                                                                                                                                                                                                                         16
                    renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is Cytomegalovirus (CMV) enhancer/Myeloproliferative sarcoma virus LTR promoter construct DNA used in the invention.
multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma),
                                                                                                                                                                                                                                                                                                         17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                   Sequence 884 BP; 229 A; 236 C; 214 G; 205 T; 0 other;
                                                                                                                                                                                                         25.4%; Score 127; DB 25;
100.0%; Pred. No. 7.9e-59;
tive 0; Mismatches 0;
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Job time : 165.871 secs
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                                                                                                                                                                                                                                        Best Local Similarity
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Appli
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                                                                                                                                                  February 15, 2004, 10:22:55 ; Search time 36.7706 Seconds
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Sequence 4
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Sequence 2
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Sequence 2
Sequence 2
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1. /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
22. /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4. /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/PcTUS_CCMB.seq:*
6: /cgn2_6/ptcdata/2/ina/PcTUS_CCMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-029-022-2
                                                                                                                                                                                                                                                                                                                                                                                                                          569978 seqs, 220691566 residues
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                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                 US-09-921-143-36_COPY_1_500
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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                                                                                                                                                        Run on:
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Sequence Sequence

Seguence

Sequence

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Sequence 287, App
Sequence 4, Applis
Sequence 33, Applis
Sequence 33, Applis
Sequence 2, Applis
                                                                               Appli
Appli
Appli
Appli
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                                                                                                         Sequence 3, A
Sequence 4, A
Sequence 11,
Sequence 287,
Sequence 288,
                                       Sequence Sequence Sequence Sequence Sequence Sequence Sequence
                Sequence :
                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08459493
Fatent No. 603658
GENERAL INFORMATION:
APPLICANT: Erigham, Kenneth
APPLICANT: Conary, John T.
APPLICANT: Canonico, Angelo
APPLICANT: Meyrick, Barbara
ITILE OF INVENTION: PLASMID FOR IN VIVO EXPRESSION
ITILE OF INVENTION: PROSTAGLANDIN SYNTHASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSES: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 S. Wacker Drive - Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 100 S. Wacker Drive - Suite 960
CITY: Chicago
STATE: 111inois
COUNTY: U.S.A.
ZIP: 60606-4002
CONPUTER READALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,493
US-09-011-745-9
US-07-678-6498-83
US-09-082-6498-83
US-09-082-6498-84
US-09-315-113-19
US-09-315-113-19
US-09-315-113-19
US-09-315-113-19
US-09-376-197-4
US-08-487-283A-3
PCT-US95-07554-4
PCT-US95-07554-4
US-09-170-496D-288
US-09-170-496D-288
US-09-170-315-4
US-08-801-092-33
US-09-313-33
US-09-313-113-33
US-09-313-113-33
US-09-313-113-33
US-09-313-113-33
US-09-313-113-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRICRATION DATA:
APPLICATION NUMBER: US 08/080,221
FILING DATE: 21-04URE-193
APPLICATION NUMBER: US 07/746,941
FILING DATE: 19-AUG-1991
ATOMER' AGANT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: VU9115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 456-8000
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 753 Dase pairs
TYPE: nucleic acid
STRANDENNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
              TOPOLOGY: circular
MOLECULE TYPE: DNA (9
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
  ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                            US-08-459-493-1
  RESULT 1
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469 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 GACTITCCIACITGGCAGIACAICIACGIATIAGICAICGCIAITACCAIGGIGAIGGGG 528
                                                                                                         77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                         529 TITITGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 588
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  17 GACTITCCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.4%; Score 127; DB 1; Length 930; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Debs, Robert J.
APPLICANT: Zhi, Ning
TITLE OF INVENTION: TRANSFECTION OF LUNG VIA AEROSOLIZED
TITLE OF INVENTION: TRANSGENE DELIVERY
NUMBER OF SEQUENCES: 4
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM SS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19930310
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,291
FILING DATE: 17 DEC 91
APPLICATION NUMBER: 972,135
FILING DATE: 05 NOV 92
APPLICATION NUMBER: PCT/US92/11008
FILING DATE: 17 DEC 92
ATTORNEY/AGENT INFORMATION:
NAME: RAG-VEGTE, BATDATA
REGISTRATION NUMBER: 32,750
REPERBNCE/DOCKET NUMBER: 05935/008001
TELECOMMUNICATION INFORMATION:
THE PROMUNICATION INFORMATION:
THE PROMUNICATION INFORMATION:
THE PROMUNICATION INFORMATION:
THE PROMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,022
FILING DATE: 19930310
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08029022
Patent No. 5641662
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 854-5277
TELEPAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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                                                                                                                                                                                                                  137 CACCCCA 143
                                                                                                                                                                                                                                                                    589 CACCCCA 595
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US-08-029-022-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Menlo Park
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-029-022-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH
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                                                                                                                                                                                                                                                                                                                                             552 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 611
                                                                                                                                                                                     17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 76
                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
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US-08-029-022-2
US-08-029-022-2
IS-08-029-022-2
| Sequence 2 Application US/08029022
| Patent No. 5641662
| GENERAL INFORMATION:
| APPLICANT: Debs, Robert J. APPLICANT: Debs, Robert J. APPLICANT: Debs, Ning
| TITLE OF INVENTION: TRANSFECTION OF LUNG VIA AEROSOLIZED
| TITLE OF INVENTION: TRANSGENE DELIVERY
| NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS: 4
| CORRESPONDENCE ADDRESS: 5
| ADDRESSEE: Fish & Richardson | STREET: 2200 Sand Hill Road, Suite 100 |
| CITY: Menlo Park | STATE: California | COUNTRY: L. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                         Query Match 25.4%; Score 127; DB 3; Length 763; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.4%; Score 127; DB 1; Length 930; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 502 or 558X
COERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,022
FILING DATE: 19930310
CLESSIFICTATION NUMBER: 809,291
FILING DATE: 17 DEC 91
APPLICATION NUMBER: 972,135
FILING DATE: 05 NOV 92
APPLICATION NUMBER: 972,135
FILING DATE: 17 DEC 91
APPLICATION NUMBER: 972,135
FILING DATE: 17 DEC 92
APPLICATION NUMBER: 972,135
FILING DATE: 17 DEC 92
APPLICATION NUMBER: 972,135
FILING DATE: 17 DEC 92
ATGORIEY/AGNIT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRALION NUMBER: 32,750
REGISTRALION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32,750
REFERENCE/OFCET NUMBER: 05935/008001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEPKX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                      612 CACCCCA 618
LOCATION: 1..763
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US-08-459-493-1
                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 TITIGGCAGIACAICAAIGGGCGIGGAIAGGGGITIGACICACGGGGAITICCAAGICIC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGGATTTCCAAGTCTC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GACTITCCTACTIGGCAGIACAICIACGIATIAGICAICGCIATIACCAIGGIGAIGCGG 76
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                                                                                                                                            Sequence 2, Application US/08246376;
Patent No. 5827703;
GENERAL INFORMATION:
APPLICANT: Robert J. Debs
APPLICANT: Ning Zhu
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.4%; Score 127; DB 1; L
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
PILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05935/005US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/92,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/84,498
FILING DATE: June 4, 1992
ATONNEY/AGENT INFORMATION:
NAME: BALBARA RABE-VENTER
REGISTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 05
TELECOMOUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                California
                             589 CACCCCA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 CACCCCA 143
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137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-246-376-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                US-08-246-376-2
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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RESULT 5

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469 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.4%; Score 127; DB 1; Length 930; Best Local Similarity 100.0%; Pred, No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
US-08-246-376-4

Sequence 4, Application US/08246376

Patent No. 2827703

Patent No. 2827703

APPLICANT: Robert J. Debs

APPLICANT: Ning Zhu
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: ALSH & Richardson
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLARASTETCATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/992,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/827,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/894,498
FILING DATE: JUNE 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/07972135
Patent No. 5858784
GENERAL INFORMATION:
APPLICANT: Robert J. Debs
TITLE OF INVENTION: GENES IN THE
TITLE OF INVENTION: GENES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:

WIDTIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 11M PS.2 Model 502 or 555X
OPRATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordferfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                                                           CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 CACCCCA 143
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US-07-972-135-2
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ORRESPONDENCE ADDRESS

LUNG BY AEROSOL - AND

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77 ITTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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Fatent No. 6001644

GENERAL INFORMATION:
APPLICANT: Ning Zhu
TITLE OF INVENTION: IS EQUENCE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPalo Alto
STREET: SPALO Alto
CTIY: Palo Alto
CTIY: Palo Alto
STREET: California
COUNTRY: U.S.A.
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25.4%; Score 127; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                              CUMPUTER: 55SX
COMPUTER: 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
SOFTWARE: 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/07/972,135
FILING DATE: No. 5888784ember 5, 1992
CLASSIFICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
APPLICATION NUMBER: 32,750
REGISTRATION NUMBER: 32,750
REGISTRATION NUMBER: 32,750
REGISTRATION NUMBER: 32,750
REFERENCE DOCKET NUMBER: 05935/007US1
TELEPHONE: (415) 854-0875
TELEPHONE: (415) 854-0875
TELEPHONE: (415) 854-0875
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                        ZOPATER: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or
          ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road,
STREET: Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-07-972-135-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-08-256-004-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.4%; Score 127; DB 2; Length 930; 100.0%; Pred. No. 2.5e-57; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                        GENES IN THE
LUNG BY AEROSOL - AND
LIPOSOME-BASED
DELIVERY
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                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road,
STREET: Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/07972135
Sequence 4, Application US/07972135
Setent No. 5858784
GENERAL INFORMATION:
TITLE OF INVENTION: EXPERSSION OF TITLE OF INVENTION: EXPERSION OF TITLE OF INVENTION: LUNG BY AEROSC TITLE OF INVENTION: LIPOSOME-BASEE TITLE OF INVENTION: LIPOSOME-BASEE NUMBER OF SEQUENCES: 4
                   LIPOSOME-BASED
DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCCCA 595
TITLE OF INVENTION:
TITLE OF INVENTION:
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469 GACTITICCIACIIIGGCAGIACAICIACGIAIIIAGICAICGCIAIIAACCAIGGIGAIGCGG 528
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25.4%; Score 127; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                               MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordberfect (Version 5.1) GURRENT APPLICATION DATA: MS/09/006,841 FILING DATE: CLASSIFICATION NUMBER: US/09/006,841 APPLICATION NUMBER: US/09/006,841 FILING DATE: No. 6468798ember 5, 1992 FILING DATE: December 17, 1991 ATTORNEY/AGENT INFORMATION: NAME: Barbara Rae-Venter REGISTRATION NUMBER: 32,750 REFERENCE/DOCKET NUMBER: 32,750 REFERENCE/DOCKET NUMBER: 32,750 REFERENCE/DOCKET NUMBER: 32,750 REFERENCE/DOCKET NUMBER: 05935/007US1 TELECOMMUNICATION: NUMBER: 05935/007US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUNG BY AEROSOL - AND
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ZIP: 94025
ZIP: 94025
COMPUTER READABLE FORM:
MEDLIM TYPE: 3.5" Diskette, 1.44 mb
MEDLIM TYPE: 3.5" MEDLIM TYPE: 3.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPOSOME-BASED
DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09006841
| Patent No. 6468798
| GENERAL INFORMATION:
| TILLE OF INVENTION: EXPRESSION OF TITLE OF INVENTION: GENER IN THE TITLE OF INVENTION: LING BY ARROSO TITLE OF INVENTION: LINGSONE-BASED:
| TITLE OF INVENTION: LINGSONE-BASED:
| TITLE OF INVENTION: LINGSONE-BASED:
| TITLE OF INVENTION: LIPOSONE-BASED:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 854-527
TELEPAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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STATE: California
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-006-841-2
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US-09-006-841-4
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COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5" Diskette, 1.44 Mb
MEDIUW TYPE: 3.5" Diskette, 1.44 Mb
MEDIUW TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02, 1994
CLASSIFICATION NUMBER: PCT/US92/11004
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/92,135
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/92,235
FILING DATE: December 17, 1991
ATPOINTEY/AGENT INPORMATION:
FILING DATE: December 17, 1991
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
ATPOINTEY/AGENT INPORMATION:
REGISTRATION NUMBER: 30,092
RELEARA (415) 843-5070
TELEFRAM: (415) 843-5070
TELEFRAM: (415) 843-5070
TELEFRAM: 930
TELEX: 030816COOLEYPA
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 930
TWINDER: 930
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25.4%; Score 127; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSION OF CLONED
GRNES IN THE
LUNG BY ARROSOL - AND
LIPOSOME-BASED
DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-06-841-2
Sequence 2, Application US/09006841
Fatent No. 6468798
GENERAL INFORMATION:
APPLICANT: ROBERT U. Debs
TITLE OF INVENTION: EXPRESSION OF
TITLE OF INVENTION: LUNG BY AEROS
TITLE OF INVENTION: LIPOSOME-BASEI
TITLE OF INVENTION: LIPOSOME-BASEI
TITLE OF INVENTION: LIPOSOME-BASEI
TITLE OF INVENTION: DELIVERY
NUMBER OF SEQUENCES;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road,
STREET: Suite 100
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-256-004-2
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529 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 588
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                                                                                                                                                                                                                                                                                                                                                                                   Length 930,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO TITLE OF INVENTION: GENE THERAPY NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESSS: ADDRESSE: 716A & Richardson STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
25.4%; Score 127; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: 1.44 Mb

COMPUTER: 1BM P6/2 Model 502 or 55SX

COMPUTER: 1BM P6/2 Model 502 or 55SX

COMPUTER: MS-DOS (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/05366

FILING DATE: 04-UUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/92,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: AMQUSE 6, 1992
APPLICATION NUMBER: 07/894,498
FILING DATE: June 4, 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05935/00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEPHONE: (415) 854-5277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9305366 GENERAL INFORMATION:
FILING DATE: June 4, 1992
ATTORNEY/AGENT INPORMATION:
NAME: BATDARA BAG-VENTER
REGISTRATION NUMBER: 32,750
                                                                                REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INPORMATION
TELEPHONE: (415) 854-0875
TELEPAX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Robert J. Debs
APPLICANT: Ning Zhu
                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-05366-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
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PCT-US93-05366-4
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GENERAL INFORMATION:

APPLICANT: Robert J. Debs
APPLICANT: Ning Zhu
TITLE OF INVENTION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES:

ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 930;
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25.4%; Score 127; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: No. 6468798ember 5, 1992
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
ATTORNEY/AGENT INFORMATION:
NAME: BATDAR RES -Venter
REGISTRATION NUMBER: 32 75
TELEPHONE: (415) 854-5277
TELEPHONE: (415) 854-6875
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1EM PS/2 Model 50Z or 55SX
COMPUTER: MS-DOS (Version 5.1)
SOPTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U893/05366
FILING DATE: 04-JUN-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/992,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: AUGUST 6, 1992
APPLICATION NUMBER: 07/894,498
                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TANNEL 930
                                                                                                                                                                                                                                                                                                                                                                                                                                  stranger acid STRANGENESS: single ; TOPOLOGY: linear US-09-006-841-4
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Agent No. 5919652
GENERAL INFORMATION:
APPLICANT: Pang, Shen
APPLICANT: Belidegrun, Arie S.
ATITLE OF INVENTION: No. 5919652el Nucleic Acid Molecules Comprising
TITLE OF INVENTION: the Prostate Specific Antigen (PSA) Promoter and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 392
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  77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                      17 GACTITCCTACTIGGCAGIACAICTACGIAITAGICAICGCIAIIACCAIGGIGAIGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 127; DB 2; I
Pred. No. 2.4e-57;
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 5919652el Nucleic Acid
TITLE OF INVENTION: the Prostate Specific Anti
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 7
CORRESSONDENCE ADDRESS:
ADDRESSEE: Merchant and Gould
STREET: 11150 Santa Monica Blvd., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 25.4%; Score 127; DB Best Local Similarity 100.0%; Pred. No. 2.4 Matches 127; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 01-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AGAISHO, SATEN B.
REGISTRATION NUMBER: 34,470
REFRENCE/DOCKET NUMBER: 3043!
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/08522841.; Patent No. 5919652
                                                                                                                                                                                                                                         ; Sequence 7, Application US/08522841
; Patent No. 5919652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                         137 CACCCCA 143
                                                                                                                                  472 CACCCCA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Los Angeles
California
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Best Local Similarity
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US-08-522-841-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Witting, Prof. Burghardt
APPLICANT: Witting, Prof. Burghardt
APPLICANT: Witting, Prof. Class
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
TITLE OF INVENTION: Therapy
FILE REFERENCE: XI 597/39
CURRENT APPLICATION NUMBER: US/09/310,842A
CURRENT FILING DATE: 1999-05-12
EARLIER FILING DATE: 1996-05-12
EARLIER FILING DATE: 1996-11-13
SOFTWARE: PAPLICATION NUMBER: 206-11-13
SOFTWARE: PATCHIN VOC: 2.1
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OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
OTHER INFORMATION: 2 can be modified with amino or caroxy features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding
LOCATION: (1077)..(1078)
OTHER INFORMATION: intramplecular binding site; the T-nucleotides at position 1077
OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 GACTITICCTACTIGGCAGIACATCIACGIATTAGICATCGCTATTACCATGGTGATGCGG
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                                                                                                                                                                                                        Length 930;
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100.0%; Pred. No. 2.5e-57;
cive 0; Mismatches 0;
                                                                                                                                                                                                   Query Match
25.4%; Score 127; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: gene
LOCATION: (1)..(1078)
OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09310842A Patent No. 6451593 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 127; Conservative
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                 LENGTH: 930
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCCCA 595
                                                                                                                                    ; TOPOLOGY: linear
PCT-US93-05366-4
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LENGTH: 1078
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US-09-310-842-1
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Search completed: February 15, 2004, 19:10:12 Job time : 40.7706 secs Sequence 25, Appl Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli Sequence 8, Appli Sequence 900, Appli Sequence 8, Appli

Sequence

Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 16, Appl Sequence 43, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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GGGATTICCAAGICICCACCCACTGACGICAATGGGAGTTIGITITGGCACCAAAAICA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TACCATGGTGATGGGGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ACGAGACTITCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAATGGGCGGGTAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAGCTTGACCTTATGCGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                publication No. US2003021592143

publication No. US2003021592141

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REPRENCE: PF112P6

CURRENT APPLICATION NUMBER: US/09/921,143

CURRENT APPLICATION NUMBER: 60/223,276

PRIOR APPLICATION NUMBER: 60/223,276

PRIOR APPLICATION NUMBER: 60/223,276

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 500; DB 13;
llarity 100.0%; Pred. No. 8.8e-272;
Conservative 0; Mismatches 0;
1 US-09-187-387-25

1 US-09-187-387-25

1 US-09-238-24-6

2 US-10-205-534-6

5 US-10-205-534-6

5 US-10-205-811-3

5 US-10-228-811-3

5 US-10-228-811-3

5 US-10-228-811-2

US-09-886-942-10

US-09-134-406-3

1 US-09-134-406-3

1 US-09-134-469-1

US-09-134-469-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                    Query Match
Best Local Simi:
Matches 500;
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Sequence 33, Appl
Sequence 425, App
Sequence 425, Appl
Sequence 68, Appli
Sequence 3, Appli
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Sequence 25, Appl
Sequence 25, Appl
                                                                                                                  February 15, 2004, 16:21:35; Search time 210.032 Seconds (without alignments) 8769.219 Million cell updates/sec
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Sequence 69, A
Sequence 2, Ap
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1: /cgn2_6/ptodata/1/pubpna/Pcr_PrubCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Pcr_Braw PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/Bcr_Braw PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-268-927-35
1 US-09-911-143-36
3 US-10-268-927-33
US-09-895-828-425
5 US-10-14-666-425
5 US-10-437-830-8
3 US-10-45-156-1
5 US-10-206-747-4
3 US-08-896-5416-33
US-10-206-747-4
3 US-08-896-25
0 US-09-2206-25
0 US-09-2206-25
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                                                                                                                                                                                                                                                                                                 2449703 seqs, 1841816367 residues
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Gapop_60.0 , Gapext 60.0
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seq length: 200000000
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Perfect score:
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Maximum DB
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327 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGATTTCCAAGTCTC 386
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Pred. No. 5.1e-61;
                                                                                                                                                                                                                       Query Match
25.4%; Score 127; DB 11;
Best Local Similarity 100.0%; Pred. No. 5.1e-61;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wain-Hobson, Simon
APPLICANT: Blancou, Philippe
APPLICANT: Chenciner, Nicole
TITLE OF INVENTION: HIV RECOMBINANT VACCINE
FILE REPRENDENC: 03495.0239-00000
CURRENT APPLICATION NUMBER: US/10/268,927
CURRENT FILING DATE: 2002-10-11
PRIOR PAPLICATION NUMBER: 06/328,449
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 544
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25.4%; Score 127; DB
Best Local Similarity 100.0%; Pred. No. 5.1
Matches 127; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/911,020A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: recombinant promoter US-10-268-927-33
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Patent No. US20020099012A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 33, Application US/10268927; Publication No. US20030175693A1; GENERAL INFORMATION:
                   2001-07-23
                   CURRENT FILING DATE: 2001-07-:
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
                                                                                                                                                        ; ORGANISM: Cytomegalovirus
US-09-911-020A-1
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                                                                                            SEC ID NO 1
                                                                                                                                  TYPE: DNA
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  181 ACGAGACTITCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240
                                                241 AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTG 300
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                                                                                            241 AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAAGCACCGTG 300
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Publication No. US20030040100A1
GENERAL INFORMATION:
APPLICANT: BROUGH, DOUGLAS E
APPLICANT: KOVESII, IMRE
TITLE OF INVENTION: CELL FOR THE PROPAGATION OF ADENOVIRAL VECTORS
FILE REFERENCE: 209459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/10268927
Publication No. US20030175693A1
GENERAL INFORMATION:
APPLICANT: Blancou, Fullippe
APPLICANT: Chenciner, Nicole
TITLE OF INVENTION: HIV RECOMBINANT VACCINE
FILE REFERENCE: 03495.0239-00000
CURRENT APPLICATION NUMBER: US/10/268,927
CURRENT FILING DATE: 2002-10-11
FRIOR APPLICATION NUMBER: 06/328,449
FRIOR FILING DATE: 2001.10-12
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 35
IENGTH: 351
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US-09-911-020A-1
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                                      APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-339
CURRENT APPLICATION NUMBER: US/09/895,828
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 473
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 425
LENGTH 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 425, Application US/10114666
| Publication No. US20030103994A1
| GENERAL INFORMATION:
| APPLICANT: Watanabe, Yoshihiro
| APPLICANT: Watenabe, Yoshihiro
| APPLICANT: Handerson, Robert A.
| APPLICANT: Kalos, Michael D.
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY | TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER | FILE REFERENCE: 210121.539C1 | CURRENT APPLICATION NUMBER: US/10/114,666 | CURRENT PILING DATE: 2002-04-01 | NUMBER OF SEQ ID NOS: 479 | NUMBER OF SEQ ID NOS: 479 | SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 127; DB 15; Length 600; 100.0%; Pred. No. 5.1e-61; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          25.4%; Score 127; DB 9; Length 600; 100.0%; Pred. No. 5.1e-61; ive 0; Mismatches 0; Indels
ang, Tongtong
McNeill, Patricia D.
Watanabe, Yoshihiro
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.4 Best Local Similarity 100. Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-09-895-828-425
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Matches 127; Conserv
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LENGTH: 600
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Sequence 68, Application US/09965703

Sequence 68, Application US/09965703

Patent No. US2002013951A1

GENERAL INFORMATION:

APPLICANT: Rohm and Haas Company

APPLICANT: Rapitekaya, Marianna Zinovjevna

APPLICANT: Cress, Dean Ervin

APPLICANT: Majutekaya, Marianna Zinovjevna

APPLICANT: Wapitekaya, Marianna Zinovjevna

APPLICANT: Cress, Dean Ervin

APPLICANT: Cress, Dean Ervin

CURRENT PRING PATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 75

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 68

LENGALL: 619
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; Bequence 3, Application US/10437830
; Publication No. US20030180949A1
; GENERAL INFORMATION:
    TPLE OF INVENTION: NUTREMEDIATES IN PLASMID PROPAGATION
    TITLE OF INVENTION: INTERMEDIATES IN PLASMID PROPAGATION
    TITLE REPERENCE: CTLIMM. 014401
    CURRENT PILICATION NUMBER: US/10/437,830
    CURRENT PILICATION NUMBER: 09/715,835
    PRIOR APPLICATION NUMBER: 09/715,835
    PRIOR PILICATION NUMBER: 09/715,835
    RICR PILICATION NUMBER: 09/715,835
    ROWERRE OF SEC ID NOS: 3
    SOFTHARE: PastSEQ for Windows Version 4.0
    SEQ ID NO 3: DENOTHE: 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
25.4%; Score 127; DB 13;
Best Local Similarity 100.0%; Pred. No. 5.1e-61;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; OTHER INFORMATION; No. US20020119521A1el Sequence
US-09-965-703-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: CYTOMEGALOVIRUS
US-10-437-830-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Cytomegalovirus
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256 GACTITICCIACITIGGCAGIACAICIACGIAITAGICAICGCIATIACCAIGGIGAIGGGG 315
                                                                                                                                                                                                                                                                                                        77 TITIGGCAGIACAICAAIGAGCGIGGAIAGCGGITIIGACICACGGGGAITICCAAGICIC 136
                                                                                                                                                                                                                                                                                                                                                           316 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
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                                                                                                                                                  Gaps
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                                                                                                  Length 884;
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COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIOR APPLICATION: «Unknown>
PRIOR APPLICATION: «Unknown>
PRIOR APPLICATION NUMBER: US 07/809,292
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/894,498
FILING DATE: 04-JUN-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/927,135
; OTHER INFORMATION; CMV enhancer/MPSV LTR promoter construct.
US-10-152-363A-69
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. L.L.W. DALLE . VO.-WV.L.YYZ

APPLICATION NUMBER: US 07/992,687

FILING DATE: 17-DEC-1992

APPLICATION NUMBER: WO PCT/US92/11004

FILING DATE: 17-DEC-1992

APPLICATION NUMBER: WO PCT/US93/05366

FILING DATE: 04-UN-1993

APPLICATION NUMBER: US 08/464,899

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: US 08/132,391

APPLICATION NUMBER: US 09/132,391

APPLICATION NUMBER: US 09/132,391

APPLICATION NUMBER: US 09/132,391
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REGISTRATION NUMBER: 46,946
REFERENCE/POCKET NUMBER: 023070-064833US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                             Query Match
25.4%; Score 127; DB 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-61;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10206747
Publication No. US20030109475A1
GENERAL INFORMATION:
APPLICANT: (1) APPLICANT:Zhu, Ning
(1) APPLICANT:Zhu, Ning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
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US-10-206-747-2
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Sequence 1, Application US/10465156

Sequence 1, Application US/10465156

Publication No. US2003023414A1

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: HYBRID VECTOR HAVING A CYTOWEGALOVIRUS

TITLE OF INVENTION: BNHANCER AND MYELOPROLIFERATIVE SARCOMA VIRUS PROMOTER

TITLE OF INVENTION: 102-15

CURRENT APPLICATION NUMBER: US/10/465,156

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: 60/389,612

PRIOR FILING DATE: 2002-06-18

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 951
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                                                        490
                                                                                                           TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGGATTTCCAAGTCTC 136
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     GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE: FEATURE: FOTHER INFORMATION: hybrid cytomegalovirus and myeloproliferative OTHER INFORMATION: sarcoma virus regulatory sequence US-10-465-156-1
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Publication No. US20030103986A1

GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
CURRENT APPLICATION NUMBER: US/10/152,363A

CURRENT FILING DATE: 2002-05-20

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: RASA
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25.4%; Score 127; DB 12; Length 8:
Best Local Similarity 100.0%; Pred. No. 5.2e-61;
Matches 127; Conservative 0; Mismatches 0; Indels
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                      CACCCCA 143
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529 TTTTGGCAGTACATCAATGGGCGTGGGTAGCGGTTTGACTCACGGGGATTCCAAGTCTC 588
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| Sequence 33, Application US/09845416
| Publication No. US20030171312A1
| GENERAL INFORMATION:
| APPLICANT: XIAO, XIAO
| TITLE OF INVENTION: DHAS SEQUENCE ENCODING A DYSTROPHY MINIGENE AND USE
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: UNMER: US/09/845,416
| CURRENT APPLICATION NUMBER: US/09/77
| PRIOR APPLICATION NUMBER: 60/200,777
| PRIOR APPLICATION NUMBER: 2000-04-28
| NUMBER OF SEQ ID NOS: 36
| SOF ID NO 33
| LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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APPLICATION NUMBER: US 09/132,391
FILING DATE: 08-No. US20030109475A1-1998
ATTOREX/AGENT INFORMATION:
NAME: MYCOÉL, Frank J.
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 023070-064833US
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                              25.4%; Score 127; DB 15;
100.0%; Pred. No. 5.2e-61;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 127; DB 13;
Pred. No. 5.2e-61;
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 930 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 127; Conservative
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CORGANISM: Homo sapiens
US-09-845-416-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-845-416-33
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                                                                                                                                                                                                                                                            Length 930;
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CITY: San Francisco
COUNTRY: USA
COUNTRY: USA
CONTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBMPC compatible
COMPUTER: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,747
FILING DATE: 11-Feb-203
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                               Query Match 25.4%; Score 127; DB 15; Best Local Similarity 100.0%; Pred. No. 5.2e-61; Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/992,687
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: WO PCT/US92/11004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-DEC-1992
APPLICATION NUMBER: WO PCT/US93/05366
FILING DATE: 04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/809,292
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/84,498
FILING DATE: 04-UN-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 06-MG-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 05-NOV-1992
    TELEFAX: (415) 576-0300
TELEX: (4UKNOWN:)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 930 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOCY: linear
MOLECTLE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhu, Ning
Zhu, Ning
TITLE OF INVENTION: Methods and (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: (i) APPLICANT:Zhu, (i) APPLICANT:Zhu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10206747 Publication No. US20030109475A1 GENERAL INFORMATION:
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; Patent No. US20020151460A1
; GENERAL INFORMATION:
APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                                                                                                                                                                                                      TITLE OF INVENTION: Method of Treating Dopaminergic and GABA-nergic Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.4%; Score 127; DB 8; Length 996; Best Local Similarity 100.0%; Pred. No. 5.2e-61; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: ONV-044.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY TIPE FORM:
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: AGCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,220C
FILING DATE: 24-Jul.-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER FOLKY, HOAG & ELIOT LLP
STREET: ONE POST OFFICE SQUARE
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-900-220C-25
                                                                                                        APPLICANT: Miao, Ningning
Wang, Monica
Mahanthappa, Nagesh K.
                                         Sequence 25, Application US/08900220C Publication No. US20020045206Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEFAX: (617) 832-7000
I FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                  Pang, Kevin
Jin, Ping
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
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RESULT 14
US-08-900-220C-25
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                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Description of Artificial Sequence: gene, OTHER INFORMATION: activation construct US-09-151-999-25
FILE REFERENCE: ONV-031.02
CURRENT APPLICATION NUMBER: US/09/151,999
CURRENT FILING DATE: 1998 08-11
EARLIER APPLICATION NUMBER: 08/955,552
EARLIER FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February 15, 2004, 22:26:45
Job time : 213.032 secs
                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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February 15, 2004, 21:50:21; Search time 1316.95 Seconds (without alignments) 9227.587 Million cell updates/sec
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1 aagcttgaccttatgcgact......cacctgggttgggatcgatc 500
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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em_gss_pro:
em_gss_pro:
em_gss_pro:
em_gss_pro:
em_gss_vrl::
gb_gssl::*
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BI489763 603032280	BI489620 603032080	BI490268 603032080	RT490467 KN20280
SUMMARIES		1 127 25.4 187 12 BI489763	BI489620	BI490268	RT490463
	DB	12	12	12	5
	Match Length DB	187	191	193	193
% 5	Match	25.4	25.4	25.4	25.4
	Score	127	127	127	127
	No.		61	о С	Ω 4

127 25.4 480 29 BZ996651 BZ996651 PUBKH7 127 25.4 500 29 BZ680401 BZ680401 PUBIS3 127 25.4 610 28 BZ680401 B68191 B68191 CIT9786K 127 25.4 619 9 AV645395 AV645395 AV64539 127 25.4 634 9 AV645390 AV645392 AV64539 127 25.4 649 9 AV641392 AV645392 AV64539 127 25.4 649 9 AV681492 AV681492 AV681492 127 25.4 651 9 AV681500 AV681500 AV68150 127 25.4 651 9 AV681500 AV681500 AV68150 127 25.4 651 9 AV681509 AV681509 AV68150 127 25.4 661 9 AV681529 127 25.4 661 9 AV68150	127 25.4 681 9 AV681512 AV681512 AV681513 AV681513	127 25.4 920 13 BX393430 BX393430 BX393430 BX393430 BX39349 BX39389 127 25.4 920 13 BX393899 BX39389 BX39389 BX39389 BX39389 127 25.4 948 13 BX364612 BX364613 BX364613 BX364614 BX366 BX689763 1 GX161616 BX68614 BX364614
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/note="Organ: pooled brain, lung, testis; Vector:
pcxv-spoRrf; Site 1: Not1; Site 2: ECCRV (destroyed); RNA
source anonymous pool of emale_brains, age range 2-7; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECCRV site is
elstroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NHH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B1490268 119 NIH_MGC_115 Home sapiens cDNA clone IMAGE:5173483 3',
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pCMV-SPORT6; Site 1: Not1; Site 2: ECORV (destroyed); RNA
source anorymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1:3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: Gapbarr@mail.mih.gov

CDN Library Preparation: Life Technologies, Inc.

CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Phttp://incygh.the.iov.column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GACTITCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                          0, Gaps
                                                                                                                                                                                                                                                                                                                                                              Query Match 25.4%; Score 127; DB 12; Length 191; Best Local Similarity 100.0%; Pred. No. 5.5e-58; Matches 127; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                /lab_host="DHIOR"
//lab_host="DHIOR"
//clone lib="WIH MGC lis"
//note="Corgan: pololed brain, lung, testis; Vector:
//note="Corgan: pololed brain, lung, testis; Vector:
//note="Corgan: pololed brain, lung, testis; Vector:
//note="Corgan: pololed brain, little="Corgan: pololed brain, last ange 23.27; lungle grant primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."
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603032080F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173483 5',
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://mage.linl.gov
Plate: LLAMIA131 row: o column: 20

High quality sequence stop: 191.
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NIH-MGC http://mgc.nci.nih.gov/.
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/organism="Homo sapiens"
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BZ996651 480 bp DNA linear GSS 25-MAR-2003 PUBKH77TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa074N10, genomic survey sequence.
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                                                                                                                            77 INTIGGCAGIACAICAAIGGCGIGGAIAGCGGITIGACICACGGGGAITITCCAAGICIC 136
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1 (bases 1 to 480)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Unpublished
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/note="Vector: pCF4_TOF0; Site_1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"
                               17 GACTITCCTACTIGGCAGIACAICTACGIATTAGTCATCGCTATTACCATGGTGATGCGG
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/strain="B73"
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BZ996651.1 GI:29240068
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//dlob=lib="NLH MGC_115"
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pcWv-sPoRT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193)
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arabed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiML at:
http://image.llnl.gov.pcolumn: 19
Plate: LLMM1431 row: p column: 19
High quality sequence etcp: 193.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Gruber (Invitrogen). Research Genetics tracking
021. Note: this is a NIH MC Library."
50 c 46 g 38 t
                                                                                                                         Score 127; DB 12; Length 193;
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25.4%; Score 127; DB 12; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-58;
Matches 127; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 5.6e
Matches 127; Conservative 0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:5173506"
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AV645385

AV645385 GLA Homo sapiens CDNA clone GLAAAG02 3', mRNA sequence.
AV645385
AV645385.1 GI:9866399
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Department of Bukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
112 Medical Center Dr., Rockville, MD 20850, USA
113.1 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Gmail: madams@tigr.org
Glones are available from Research Genetics (info@resgen.com). BAC end.search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T?
Class: BAC ends.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 619)

Xia,X., Haung,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,P., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,

Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver accinoma
with those of corresponding noncancerous liver

21625106
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Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tal: 86-21-50801919(ex.45)
Fas: 86-21-50801925
Email: hanzgechgc.8h.cn
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                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
mol_type="genomic DNA"
Mb_xref="gDB:726476"
/db_xref="taxon:9606"
/clone="A-492C12"
                                                                                                                                                                                                                                                     Location/Qualifiers
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1 (bases 1 to 610)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H., Simon, M. and Venter, J.C.
Simon, M. and Venter, J.C.
Building
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/organism="Zea mays"

/ord_lrype="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/db_xref="taxon:4577"

/dclone="zmMBTa064H03"

/clone=lib="ZmMBTa064H03"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high

COT selected genomic DNA library"

a 129 c 120 g 128 t
                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Maize Genomics Consortium
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genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA
18-1: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Other_GSSs: CIT978SK-A-492C12.TP
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                                                                            BZ680401.1 GI:28235262
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AV645392 GLA Homo sapiens cDNA clone GLAAAG09 3', mRNA sequence.
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Ku,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,X., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
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    'note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Ruman Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Eax: 86-21-50801912
Email: hanzgochgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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'dev_stage="Adult"
'lab_host="SOLR"
                                                                                                                                                                                                                                                                                                        324 TITTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCCACGGGGATITCCAAGTCTC
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100.0%; Pred. No. 6.8e-58;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="GLAAAG09"
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Matches 127; Conservative
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Best Local Similarity 100.0
Matches 127; Conservative
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1. (Dases I to 634)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, O., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                          /clone_lib="GLA"
|note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                            'tissue type="corresponding non cancerous liver tissue"
'dev stage="Adult"
'lab_host="SOLR"
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This clone is available at CHGC in Shanghai. Location/Qualifiers
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lone is available at CHGC in Shanghai.
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Pred. No. 6.8e-58;
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                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAAG02"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAAG07"
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lab_host="SOLR"
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AV681500
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 RESULT 12
AV681492/c
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AV645393 GLA Homo sapiens cDNA clone GLAAAG10 3', mRNA sequence.
AV645393
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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385 GACTITCCTACTIGGCAGIACATCTACGIATIAGICAICGCTAIIACCAIGGGAIGGIGAIGCGG 326
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 640)
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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/dev_stage="Adult"
/lab_host="SOLR"
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100.0%; Pred. No. 6.8e-58;
iive 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAAG10"
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This clone is available at CF
Location/Qualifiers
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Homo sapiens (human)
Homo sapiens
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Matches 127; Conservative
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AV645393/c
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AV681500 GXA Homo sapiens CDNA clone GXAAAD08 5', mRNA sequence.
AV681500 AI:10283363
AV681492 GXA Homo sapiens CDNA clone GKAAAD01 5', mRNA sequence.
AV681492 AX HOMO SAPISS CDNA CLONE GKAAAD01 5', mRNA sequence.
AV681492.1 GI:10283355
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I (Dases I to 648)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, X., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15094 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo.
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/db_xref="emrNA"
/clone="GT&AADO1"
/fiseue_type="hepatocellular carcinoma"
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Homo sapiens
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AV681509 GKA Homo sapiens cDNA clone GKAAAC02 5', mRNA sequence.
AV681509
Fax: (617) 632-6989
Email: thomas look@dfci.harvard.edu
Email: thomas look@dfci.harvard.edu
The clone was obtained from an R2DD array made from an adult kidney
cDNA random primed library from Leonard Zon. RZPD library number
576. This clone is available from the Resource Centre/Primary
Database of the German Human Genome Project: RZPD (Ressourcen
Sentrum Primr Datenbank). http://www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 530
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Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 661)
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Chinese National Human Genome Center at Shanghai
315 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
20123, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.8h.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                      // Organism="Danio rerio"
//organism="Danio rerio"
//organism="Danio"/
//organism="Danio"/
//organism="Serio"/
//organ="Reportation of the configuration of 
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llarity 100.0%; Pred. No. 6.8e-58;
Conservative 0; Mismatches 0;
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pediatric Oncology Department, Mayer Building-630, 44 Binney Street, Boston, MA 02115, USA
Tel: (617) 632-5826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Shao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancercus liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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note="Vector: pBluescript sk(-); Site_l: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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tive 0; Mismatches 0;
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Dana-Farber Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 g
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AUTHORS
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362 TITIGGCAGTACATCAATGGGGCGTGGATAGCGGTTTGACTCACGGGATTTCCAAGTCTC 303
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clone="GKAAAC02"
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	Run on: February 15, 2004, 19:10:26; Search time 3961.99 Seconds (without alignments) 10335.846 Million cell updates/sec	Title: US-09-921-143-36_COPY_2000_3000 Perfect score: 1001 Sequence: 1 tctcaggctaaccagtggggttcggctgcggcgagcggta 1001	Scoring table: OLIGO NUC Gapop 60.0, Gapext 60.0	Searched: 2888711 segs, 20454813386 residues	Word size : 0	Total number of hits satisfying chosen parameters: 5777422	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 45 summaries	Database : GenEmbl:* 1	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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N m	494		1146		INS2	1243 Rat gene
4-го	358 358		3980		A30511 A30509	A30509 Plasmid p26
ψt	343	* 0	2852		RATINSII	J00748 Rat insulin
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25	290		738		AR141144	AR141144 Sequence
26	290	ο,	738		AR181919	Sequence
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ACCESSION		98563		9		
ເດ ⊁		HTG; HTGS Rattus nor	PHASE2	HTGS:	S14'1 HTGS_DRAFT; HTGS_FULLTOP (Norway rat)	, Cu
ORGHINION		Eukaryota Mammalia,	Wetazo Eutheri		Chordata, Craniata, Ve Rodentia, Sciurognathi	Vertebrata; Buteleostomi; hi; Muridae; Murinae;
REFERENCE	Rat 1	Rattus. 1 (bases 1 Muzny D Marri	1 to 2.	7893 Vet 7	to 278936) - Metzker M Lee . Abramzon .	
SACHION	All	en, c.,	Allen, H.,		Alsbrooks, S., Amin, A.,	Anguiano, D.,

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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldein, D., Bandaranarke, D., Barber M., Barnstead, M., Benahmed, P., Biswalo, K., Blanke, D., Barber M., Barnstead, M., Benahmed, P., Biswalo, K., Blanke, D., Barber M., Barnstead, M., Benahmed, P., Biswalo, K., Blanke, D., Barber, M., Blyth, P., Brown, M., Carderon, E., Cardeno, V., Carter, K., Cankeron, E., Cardeno, V., Carter, K., Cankeron, E., Cardeno, Y., Carter, K., Cankeron, E., Cardeno, V., Carter, K., Cankeron, E., Chen, E., Chen, Y., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Che
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23664519.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs are ordered and oriented, and separated by sized gaps filled with Storm to the consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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COMMENT

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47535 AACAGGATGTGTAGGTTTTTGGAGGCCCATATGTCCATGACCAGTGACTTGTCTCAC 47594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGCTGCCAGGAAGGAGTGAGAATCCTTCCTTAAGTCTCCTAGGTGGTGGTGACGGGTGGCTAG 120
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                                                                                                                                                                          Assembly program: Atlas 3.0;
Consensus quality: 257140 bases at least Q40
Consensus quality: 257143 bases at least Q30
Consensus quality: 257743 bases at least Q30
Estimated insert size: 269272; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCCCCAGGATAGGTACCTATTTGGGGACCCCATAGAGCACTGCACTGAGGGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AACAGGAIGIGIAGGITTIGGAGGCCCATAIGICCAITCAIGACCAGIGACTIGICICAC
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
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277874, .278936
/note="wgg_contig"
1 64123 c 64880 g 63888 t 20450 others
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Center: Baylor College of Medicine
Center: Cade: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: pgsc.help@bcm.tmc.edu
Center: project Information
Center project name: GIKN
Center clone name: GTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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/note="wgs_end_extension
clone_end:Sp6"
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276008. .277823
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/note="clone_boundary
clone_end:Sp6
site:EcoRI
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17595 AGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAAAAGCCTG 47654
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Rattus norvegicus clone CH230-57B2, WORKING DRAFT SEQUENCE, 6
unocdered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                           47715 GTGCTGCTGATGCTCTGCCCTGTGCTGACATGACCTCCCTGGCAGTGGCACACACTGGAC
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Morgavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, D., Perac, D., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, J., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Revilli, E., Reves, K., Regiter, M., Reilly, M., Ren, Y., Reuter, M., Rose, R., Ruiz, S., Shen, H., Sander, W., Savery, G., Scherer, S., Sock, T., Riggs, F., Rives, C., Royery, G., Scherer, S., Sock, G., Shatsman, S., Shen, H., Sheety, J., Shvartsbeyr, A., Sisson, I., Sitter, C.D., Smajs, D., Sheity, J., Shvartsbeyr, A., Suston, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Waright, D., Willson, S., Yakub, S., Yen, J., Yoon, V., Willson, W., Miczyk, R., Wocken, H., Worley, K., Wight, D., Wright, D., Wright, D., Wright, D., Wright, D., Wright, D., Von, V., Zhao, S., Dunn, D., Von, N., Valas, R., Smith, D., Von, Niederhausern, A., Weiss, R., Molt, R., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL SUBMILTER (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

Of May 10, 2003 this sequence version replaced gi:23664548.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (Ittp://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Direct Submission
Submitted (15-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 288862)
Rat Genome Sequencing Consortium.
Direct Submission Annal Genome Asemuencing Center, Department
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Consensus quality: 253655 bases at least Q30
Consensus quality: 253157 bases at least Q30
Estimated insert size: 275631; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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------ Summary Statistics
Assembly program: Atlas 3.0;
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1 (bases 1 to 1146)
Lomedico.P., Rosenthal,N., Efstratidadis,A., Gilbert,W.,
Kolomer,R. and Tizard,R.
The structure and evolution of the two nonallelic rat preproinsulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(219. .404,904. .1050)
/codon_gtart=1
/product="preproinsulin"
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ERGFFYTPMSRREVEDPQVAQLELGGGPGAGDLQTLALEVARQKRGIVDQCCTSICSL
                                                                                                                                                                                                                                     ROD 09-APR-1993
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    GAGCACTACAAGTIGIGIGIACAIGCGIGCAIGIGCAIAIGIGGIGCGGGGGGGAACAIGA 660
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                                                                                                                                                                                                                                                                                          V01243.1 GI:56489
insulin; preproinsulin.
Kattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCAGGCTAACCAGTGGGGGCCACATTTCTGTGGGCAGCTAGACATATGTAAACATGGT
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Pred. No. 6.4e-278;
0; Mismatches 3;
                                                                                                                                                                                                                                     DNA
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                     1146 bp
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/number=3
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/number=2
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/number=1
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Best Local Simil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226182
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it is available and the accession number will
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                                 281936: contig of 281836 bp in length
837 281936: gap of unknown length
837 282992: contig of 1056 bp in length
993 282992: gap of unknown length
136 284135: contig of 1043 bp in length
136 284235: agp of unknown length
136 285479: contig of 1144 bp in length
1380 285479: contig of 1144 bp in length
1380 285479: contig of 1144 bp in length
1380 285479: contig of 1149 bp in length
1380 285479: contig of 1189 bp in length
1381 28862: contig of 1999 bp in length
1382 28863: contig of 1799 bp in length
138862: contig of 1799 bp in length
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55666 c 58691 g 65812 t 33147 others
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100.0%; Pred. No. 0;
ive 0; Mismatches 0
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complement(280810, .281
/note="clone_boundary
clone_end.sp6
site:EcoR1
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Best Local Similarity 100.
Matches 679; Conservative
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	ONA linear PAT 0	Soluble interferon-gamma receptors and m Parent: EP 0393502-A 76 24-0CT-1990; F. HOFFNANN LA ROCHE AG Location/Qualifiers 1. 398 / Acganism="synthetic construct" / mol_type="genomic DNA" / Abzref="taxon:32630" 947 a	131 GAGGGATGGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGA 23 171 GAGGGATGGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGA 23 174 GAGGGATGGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGA 93 175 CTTGTCTCACAGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGATAAAGTGAG 29 176	0y 291 AGAAAGCCTGGGCTAATCAGGGGGTCGCTCAGCTGCATTGTCCTAACTGGTTTGTTGTT 350
	OY 481 AGCGCGCATCGTGGATCAGTGCTGCACCACATCTGCTCTCTACCAACTGGAGAACT 540 Db 980 AGCGCGGCATCGTGGATCAGTGCTGCACCAGCATCTGTCTCTCTACCAACTGGAGAACT 1039 Qy 541 ACTGCAACTAGGCCCACCACTACCTGTCACTCTCTCTCTACCAATGAATAAAACTTTGAAA 600 Db 1040 ACTGCAACTAGGCCCACCACTACCTGTCCACTGCAATGAATAAAACCTTTGAAA 1099 Qy 601 GAGCACTACAAGTGTGTGTGTACATGCGTGCATGTGGTGC 647 1100 GAGCACTACAAGTTGTGTACATGCGTGCATGTGTGTGGTGC 1146	r PAT 05-JUL-20	JOURNAL PATENT: PROJECTOR JOURNALD PATENT: PLOUDCING ACCURAGE AG FEATURES F. HOFFMANN-LA ROCHE AG FEATURES JOSEPH F. HOFFMANN-LA ROCHE AG JOURNES JOSEPH F. HOFFMANN-LA ROCHE AG JOURNES JOSEPH F. HOFFMANN-LA ROCHE AG JOURNES JOURNE	Ouery Match Best Local Similarity 99.6%; Pred. No. 5e-198; Matches 458; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 171 GAGGGATGGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGA 230

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/note="insulin II signal peptide"
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99.4%; Pred. No. 3.3e-189;
tive 0; Mismatches 3;
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/product="insulin II B-chain"
1881. .1943
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/product="insulin II A-chain"
<1115. .1301
                    'organism="Rattus norvegicus"
'mol type="qenomic DNA"
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/note="ins-II mRNA intron A"
/note="preproinsulin II"
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'note="ins-II cds intron
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/note="preproinsulin II"
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/note="ins-II mRNA [1]"
                                        /mol_type="genomic DNA
/db_xref="taxon:10116"
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In a personal communication, S.Chan [4] noted that the 5' end of the sequence in fig. 5 of [2] is incorrect; hence we have only included the bases 3' to this area.

A TATA box is located at positions 909-914, and a poly-A signal at 1980-1985.
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Lomedico,P., Rosenthal,N., Efstratidadis,A., Gilbert,W.,
Kolodner,R. and Tizard,R.
The structure and evolution of the two nonallelic rat preproinsulin
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                                                                                                                                                   1174 GCCCGGCAGAAGCGCGCGCATCGTGGATCAGTGCTGCACCAGCATCTGCTCTCTACCAA 1233
1114 CAACTGGAGCTGGGTGGAGGCCCGGGGGCAGGTGACCTTCAGACCTTGGCACTGGAGGTG 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus (Abraka) (Kaniata, Vertebrata; Euteleostomi;
Eukaryota; Metazoa; (Hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1984)

5 (bases 1 to 2852)

Sources,M.B., Schon,E., Henderson,A., Karathanasis,S.K., Cate,R., Zeitlin,S., Chirgwin,J. and Efetratiadis,A.

ENNA-mediated gene duplication: the rat preproinsulin I gene is a functional retroposon

Mol. Cell. Biol. 5 (8), 2090-2103 (1985)
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                                          GCCCGGCAGAAGCGCGCATCGTGGATCAGTGCTGCACCAGCATCTGCTCTCTTACCAA
                                                                                                                             CTGGAGAACTACTGCAACTAGGCCCACCACTACCCTGTCCACCCCTCTGCAATGAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chan, S.J., Noves, B.E., Agarwal, K.L. and Steiner, D.F. Construction and selection of recombinant plasmids containing full-length complementary DNAs corresponding to rat insulins I
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80056629
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Rat insulin II gene (ins-2) with two introns.
J00748.
J00748.1 GI:204958
insulin.
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80045035
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Unpublished (1984)
4 (bases 1103 to 1228)
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linear PAT 10-APR-2003
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1 (Dases 1 to 584)
Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S., Carter,D., Retter,M.W., Mannion,J. and Fan,L.
Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
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/organism='pUC 18'.
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/organism="unidentified"
/or_type="genomic DNA"
/db Zref="taxon:32644"
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                                                      Ricin-like toxin variants for treatment of cancer, viral or parasitic infections.
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/organism≈'Baculovirus transfer vector pVL
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Best Local Similarity 100.0%; Pred. No. 1.1e-158;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                         unclassified.

1 (bases 1 to 9632)

BorgCord, T.

Ricin-like toxin variants for treatment of cancer, viral or parasitic infections

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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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30-APR-1997 US 60/04514
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JP 2001523961-A/1.
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JP 2000159768-A/2.
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Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION (US)
Location/Qualifiers
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CORIXA CORPORATION (US)
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                                AX063012
Sequence 639 from Patent W00100828.
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                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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Sequence 639 from Patent
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AX367929.1 GI:18856016
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Unclassified.
1 (bases 1 to 584)
1 (bases 1 to 584)
Wang, T., Bangur, C.S., Lodes, W.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.
Compositions and methods for the therapy and diagnosis of lung
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                                                                                712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
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                                     4.6e-158;
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Sequence 639 from patent US 6509448.
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Matches 290; Conservative 0; Mismatches
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Unclassified.

1 (bases 1 to 701)
Chatterjee,D.K.
Cloned DNA polymerases from thermotoga maritima and mutants thereof Patent: US 5948614-A 24 07-SEP-1999;
Location/Qualifiers
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211 ATTAATGAATCGGCCAACGCGCGGGAGGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 270
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Unclassified.
1 (bases 1 to 701)
Hughes, A.J. and Chatterjee, D.K.
Cloned DNA, polymerses from Thermotoga and mutants thereof
Patent: US 6506560-A 24 14-7AN-2003;
Patent: Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.6e-158;
Matches 290; Conservative 0; Mismatches 0;
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Sequence 24 from patent US 6506560.
AR274302
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Sequence 24 from patent US 5948614.
AR072501. GI:9999265
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 126 from Patent WO0196390.
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Best Local Similarity 100.0%; Pred. No. 4.6e-158; Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps
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(c) 1993 - 2004 Compugen Ltd.
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	Description	Expression vector	Sequence of plasmi	pDIP/PyCSP.1 plasm	Baculovirus transf	Baculovirus transf	Human prostate exp	Fragment #2 of pUC	N. meningitidis pa
SUMMARIES	ΩI	ABK10062	AAQ06312	AAA58309	AAT97898	AAX04251	ABV45293		
		24	11	21	18	20	23	21	21
	% Query Match Length DB	5283	3979	5552	9632	9632	409	450	515
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(HUMA-) HUMAN GENOME SCI INC. 04-AUG-2000; 2000US-223276P. 03-AUG-2001; 2001WO-US24658.

Coleman TA;

	ď	cDNA encoding clon	Human lung neuroen	Lung cancer therap	Human breast cance	Orestes sequencing		Human nervous syst			Human reproductive	DNA encoding novel	Human immune/haema	coding huma	testicular	uman secreted pr	protein	Secreted protein g	secreted	Human secreted pro	. meningitidi	T. neapolitana Tne	N. meningitidis pa	N. meningitidis pa	Plasmid pGEM DNA f	Human immune/haema	Human ovarian tumo	E. coli J96 pathog	Human cDNA 5'-end	Human cDNA clone r	Porcine muscular s	ø	Human prostate can	moter s	an prostat	DNA encoding novel
ABV45308	AAF68704	ABK38615	ACA10944	ABX99895	AAA62566	ABT12681	ABK27689	ABA20358	ABA21448	AAL05999	AAL07025	AA\$27722	AAK87476	AAS33387	ABL98563	ABK69910	ABZ74009	ABZ74600	ABZ68007	ABZ68121	AAA81954	AAZ88769	AAA81967	AAA81752	AAZ09716	AAK61981	AAH82483	AAV31294	AAK91757	AAK93193	AAS61891	AAZ97398	AAZ97334	AAC83524	AAZ97209	ABK43594
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ALIGNMENTS

ABK10062

Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1; chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a; allergic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferative disorder; viral infection; bacterial infection; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; gene therapy. Expression vector construct pVGI.1 containing VEGF-2 insert. ABK10062 standard; DNA; 5283 BP. (first entry) WO200211769-A1. 14-FEB-2002. 21-MAY-2002 Synthetic. ABK10062;

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expression vector construct containing the vacular endothelial growth factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell with the DNA and for transforming or transfecting ischaemia or myocardial ischaemia, or a disease or disorder selected from autoimmune disorders (e.g. rheumatoria arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease), cardiovascular disorders (e.g. cardiowascular disorders (e.g. cardiowascular disorders and embolism. This sequence represents the PVGI-1 expression vector containing the VEGF-2
                                          Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischaemia or myocardial ischaemia, autoimmune disorders and allergic
                                                                                                                                                                                                                      invention relates to an isolated nucleic acid comprising pVGI.1
                                                                                                                                                                      Disclosure; Fig 31; 241pp; English.
                                                                                                                        conditions
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Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 other;

0; Gaps Query Match 100.0%; Score 1001; DB 24; Length 5283; Best Local Similarity 100.0%; Pred. No. 6.8e-300; Atches 1001; Conservative 0; Mismatches 0; Indels 0;

2179 2059 240 2119 180 120 2000 TCTCAGGCTAACCAGTGGGGGGCACATTTCTGTGGGCAGCTAGACATATGTAAACATGGT TCTCAGGCTAACCAGTGGGGGCACATTTCTGTGGGCAGCTAGACATATGTAAACATGGT AGCTGCCAGGAAGGAGTGAGAATCCTTCTTAAGTCTCCTAGGTGGTGACGGGTGGCTAG 2060 AGCTGCCAGGAAGGAGTGAGAATCCTTCCTTAAGTCTCCTAGGTGGTGACGGGTGGTGGTGAC AACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCAC Н 181 61 g δ 셤 ò g ઠે d 8

2180 AACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCAC 2239 241 AGCCATGCAACCCTTGCCTCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTG 300 × 2240 AGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTG

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2600 GAGCACTACAAGITGIGIGIGIACAIGCGTGCAIGTGCATAIGTGGCGGGGGGAACAIGA 2659

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AAQ06312 standard; DNA; 3979 BP RESULT 2 AAQ06312

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AAQ06312;

(updated)
(first entry) 25-MAR-2003 29-JAN-1991

Sequence of plasmid p264BGL.

IFN-gamma receptor; autoimmune disease; multiple sclerosis; hypersensitivity; ds.

Location/Qualifiers ۲. /*tag= c /label= S.F 1288..1292 /*tag= d 243..426 /*tag= b 279..242 243..405 *tag= *tag= Homo sapiens, polyA_signal Sig-peptide Key CDS

(HOFF) HOFFMANN-LA ROCHE AG. 90EP-0106992 90EP-0106992 11-APR-1990; 11-APR-1990; 24-OCT-1990

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EP393502-A.

Stuber D; Fountoulakis M, Garotta G, WPI; 1990-322042/43.

P-PSDB; AAR07066

900

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Soluble interferon-gamma receptors - for treating auto-immune diseases, chronic inflammations, etc.

Disclosure; Fig 55; 174pp; English.

Hedstrom RC

Sedegah M, Hoffman SL,

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1024 GCTCCTCCTAACTGGATTGTCCTATGTGTCTTTGTGCTTCTGTGCTGCTGATGCTCTGCCCT 1083
                                                                                                                                                                                                                                                                                                                             1084 GTGCTGACATGACCTCCCTGGCAGTGGCACAACTGGAGCTGGGAGGCCCGGGGGCAG 1143
                                                                                                                                                                                                                                                    441
                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                                                                                                                                                                      561
                                                                                                                                                                                          322 GCTCCTCCTAACTGGATTGTCCTATGTGTCTTTGCCTTCTGTGCTGCTGATGCTCTGCCCT 381
                                                                                                                                                                                                                                                                                                                                                                                                                             562 ACCUTGUCCACCCCTCTGCAATGAATAAAACCTTTGAAAGAGCACTACAAGTTGTGTGTA 621
                                                                                                                                                                                                                                                 382 GIGCTGACATGACCTCCCTGGCAGTGGCACACAGCTGGAGCTGGAGGCCCGGGGGCCAG
                                                                                                                                                                                                                                                                                                           442 GIGACCTICAGACCTIGGCACTGGAGGTGGCCCGGCAGAAGCGCGGCATCGTGGATCAGT
                                                                                                                                                                                                                                                                                                                                                                      502 GCTGCACCAGCATCTGCTCTCTCTACCAACTGGAGAACTACTGCAACTAGGCCCACCACT
                                                                                                                                                                Gaps
IFN-gamma is a therapeutically active agent in the treatment of autoimmune disease, allograft transplant rejections, multiple sclerosis, chronic inflammations and delayed hypersensitivity. It is also useful in identifying IFN-gamma agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pDIP/PyCSP.1 plasmid; malaria vaccine; circumsporozoite protein;
protozoacide; immunoenhancer; human; rat; ds.
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                                                                                                                            Query Match 30.9%; Score 309; DB 11; Length 3979; Best Local Similarity 100.0%; Pred. No. 8e-87; Matches 309; Conservative 0; Mismatches 0; Indels 0;
                                                                                                  Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "IL-2 PyCSP fusion protein"
                                                                       (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pDIP/PyCSP.1 plasmid nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "CMV-IE promoter'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA58309 standard; DNA; 5552 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0155888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       933..2369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1324 CATGCGTGC 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622 CATGCGTGC 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2000.
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2759 CTTGTCTCACAGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAG 2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2939 CAACTGGAGCTGGGTGGAGGCCCGGGGCCGGTGACCTTCAGACCTTGGCACTGGAGGTG 2998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2999 eccescacada accecaca regresar carecración es case accecacamente de contra con contra con contra con contra con contra con contra con contra cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3059 CTGGAGAACTACTGCAACTAGGCCCACCACTACCCTGTCCACCCCTCTGCAATGAA 3118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the plasmid vector pDIP/PyCSP.1. The vector comprises a gene encoding Plasmodium yeeli dircumsporozoite protein (PyCSP), operably linked to promoter from Cytomegalovirus (CMV.IE). The expression of the CSP gene results in the production of an immune response to the malaria protein and a reduction in malaria parasites at the pre-erythrocytic, erythrocytic, and gametocyte stages of infection. The present sequence can therefore be used as a malaria vaccine. The present sequence has human and rat components also: partial human IL-2 sequence and partial rat preproinsulin II sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 GAGGGAIGGIAACAGGAIGIGIAGGIIIIIGGAGGCCCATAIGICCAIICAIGACCAGIGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AGAAAGCCTGGGCTAATCAGGGGGTCGCTCAGCTCCTCCTAACTGGATTGTCCTATGTGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 CAACTGGAGCTGGAGGCCCGGGGGCAGGTGACCTTCAGACCTTGGCACTGGAGGTG 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 CITGICICACAGCCAIGCAACCCITGCCICCIGIGCIGACTIAGCAGGGGAIAAAGIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 CTTTGCTTCTGTGCTGCTGATGCTCTGCCCTGTGACATGACATGACCTCCCTGGCAGTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2819 AGAAAGCCTGGGCTAATCGGGGGGGCTCCTCCTCCTAACTGGATTGTCCTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                      Inducing protective immune responses against Plasmodium parasite proteins for controlling malaria in mammala comprises injecting a polymuciaeotide delivery vector having a DNA sequence coding for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ricin; toxin; antiviral; virucide; retrovírus; protease; HTLV-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.7%; Score 307; DB 21; Length 5552; Best Local Similarity 99.3%; Pred. No. 2.9e-86; Matches 457; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5552 BP; 1605 A; 1303 C; 1321 G; 1323 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Columns 15-22; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baculovirus transfer vector pVL1393.
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                                                                                                                           WPI; 2000-410681/35
                                                                                                                                                                                                                                                                                                                                                                             Plasmodium protein
                                                                                                                                                                      P-PSDB; AAB07288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4302 ACGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACAC 4361
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the DNA sequence of baculovirus transfer vector pVL1393.
A claimed baculovirus transfer vector incorporates a nucleic acid (see AAT97899-901, AAT97910, AAT97915, AAT97916 and AAT97919) that encodes a recombinant protein in which the A and B chains of a ricin-like toxin are linked by a heterologus linker peptide (see AAM96880-86) that contains a cleavage recognition site for a retroviral protease such as HIV, HTLV-1 or HTLV-1. The vector provides expression of the recombinant proteins in Sf9 insect cells. The recombinant proteins can be used to selectively inhibit or destroy mammalian cells infected with a retrovirus, such as cancer cells associated with HIV or cells associated with HIV. The recombinant proteins are non-toxic until the ricin A chain is liberated from the B chain by the retroviral protease, and thus can be used to specifically target infected cells without the need for a cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 ACGTAATCATGGTCATAGCTGTTTCCTGTGTAAATTGTTATCCGCTCACAATTCCACAC 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     831 ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               891 CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGGCT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                 DNAs encoding ricin like toxins A and B - are linked via linker containing cleavage site for retroviral protease, used to inhibit or destroy mammalian cells infected with retrovirus
cancer, infection; therapy; vector; pVL1393; ds; circular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951 TCCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGGCGGGGGTA 1001
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100.0%; Pred. No. 2e-81;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9632 BP; 2602 A; 2122 C; 2176 G; 2732 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Fig 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX04251 standard; DNA; 9632 BP
                                                                                                                                                                                           96US-0016509.
                                                                                                                                                     97WO-CA00288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 291; Conservative
                                                                                                                                                                                                                                (CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                               WPI; 1997-549735/50.
                                                                                                                                                     29-APR-1997;
                                                                          WO9741233-A1
                                                                                                                                                                                           30-APR-1996;
                                                                                                                 06-NOV-1997.
                                    Baculovirus.
                                                                                                                                                                                                                                                                      Borgford T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   component.
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The present invention describes new purified and isolated nucleic acids

(II) encoding: (1) the A and B chains of a ricin-like toxin (II); and

(II) a heterologous linker, joining the two chains and including a

cleavage recognition site for a disease specific protease (III). Also

described are: (1) plasmids or bacalcovins transfer vectors that contain

(I); and (2) recombinant protein (IV) consisting of the A and B chains

of (II) joined by the specified linker. (IV), produced by expression of

(I) in host combinant protein (IV) consisting of the A and B chains

of (III) particularly for treating cancers (e.g. leucocyte

produce (III), particularly for treating cancers (e.g. leucocyte

proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or

infections caused by fungi, parasites (e.g. milaria) or viruses (e.g.

cytomogalovirus (CMV), herpes, hepatitis, rhimovirus, laryngeotracheitis,

poliomyelitis or varicella zoster), also cystic fibrosis and multiple

colleonyelitis or varicella zoster), also cystic fibrosis and multiple

colleonyelitically for (III)-expressing cells and does not depend for

specificity on a cell-binding component. When used to rreat viruse

concertorade translocation from endoplasmic reticulum to cytoplasm (which

come viruses exploit to avoid immune detection), so eslectivity and

safety are further improved. (IV) are not toxic until chain A is

released and this occurs only in target cells. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7002 acchaarcarcaracararacrerrrecrereneaaarrerrarececreacaarrecacae 7061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831 ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    711 ACGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding ricin-like toxin with an interchain linker cleaved by protease - is specific for diseased cells, useful for, e.g. killing selectively cancer or infected cells
                                                                         Ricin-like toxin, cancer, viral infection, parasitic infection, linker, B chain; A chain; protease, fungal infection; malaria; leucocyte proliferation; cytomegalovirus; herpes; hepatitis; rinnovirus; laryngeotracheitis; polionyelitis; varicella zoster; cystic fibrosis; multiple sclerosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%; Score 291; DB 20; Length 9632; 100.0%; Pred. No. 2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents a nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9632 BP; 2602 A; 2122 C; 2176 G; 2732 T; 0 other;
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                                         Baculovirus transfer vector pVL1393 DNA sequence.
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97US-0045148.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-009431/01.
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                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                        WO9849311-A2
                                                                                                                                                                                                                                                                                                                                                        30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1997;
  15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1997;
                                                                                                                                                                                                                                                                                                                 05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borgford T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                    832
                                                                                                                                                  226
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                                                                                                                                                                                                                                                                                                               RESULT
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                             7182 CATTAATGAATCGGCCAACGCGGGGGGGGGGGGTTTGCGTATTGGGCGCTCTTCCGCT 7241
    7122 ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG 7181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                               Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         state cells and correlating with presence of prostate cancer, useful detecting presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state

    is also useful as a pharmacodyanamic or pharmacogenomic marker

                                                                                                              7242 TCCTCGCTCACTGACTCGCTGCGCTCCGTCGTTCGGCTGCGGCGAGCGGTA 7292
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                                  CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
                                                                                                                                                                                                                                                                                    expression marker cDNA 45284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monahan JE;
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                                                                                                                                                                                                 ABV45293 standard; cDNA; 409
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                                                                                                                                                                                                                                                                                       prostate
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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for detect
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This sequence is a fragment of the pUC 18 nucleotide sequence. The fragments is used in the course of the invention. The invention relates to pyrrole derivatives which recognise a specific DNA base sequence, and strongly bind to the adjacent base via a covalent bond. The pyrrole derivatives alkylate the base sequence, once it has been recognised. The invention also relates to an agent (made from the pyrrole derivatives) for alkylating genes, a process for producing an agent for alkylating genes, and a method for regulating the expression of a gene with a part containing the specific base sequence comprising using an alkylating agent. The compounds are useful in drug compositions for regulating expression of a gene carrying a base sequence which can be recognized then alkylated by them, e.g. in treatment of cancers.
 165
                                                                                                                                              285
                                                                                                                                                                                   951
                                                                                                                                                                                                                   ATTAATGAATCGGCCAACGCGGGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 345
                                     831
                                                                      225
                                                                                                           891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrrole derivative; DUC 18; alkylating agent; gene expression regulator; treatment; drug; cancer; ds.
                                                                                                           CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
106 ceraarcareercaraecrerrrecrereraaarrerrareeecreaarrecaea
                                                                    ATTAATGAATCGGCCAACGCGCGGGAGAGGCGCGTTTGCGGTATTGGGCGCTCTTCCGGCTT
                                     New pyrrole derivatives for alkylating specific base sequence of DNA, useful in drug compositions for regulating expression of a gene carrying a base sequence which can be recognized then alkylated by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragment #2 of pUC 18 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    them, e.g. in treatment of cancers -
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29.0%; Score 290; DB 21; Length 450;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes methods of obtaining immunogenic proteins from Veisseria genomic sequences. AAAB1453 to AAAB2114 represent specifically claimed Naisseria meningitidis genomic DNA sequences, AAAB1260 to AAAB150 to AAAB150 to AAAB160 to AAAB1303 and AAB25620 to AAB2563 represent Neisseria DNA sequences and their corresponding proteins, AAAB1254 to AAAB1259 and AAAB1304 to AAAB1321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1252 represent Neisseria meningitidis Memb Polymucleoride ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies
                                                                                                                                                                                                                 832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tettelin H, Venter JC;
Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                                      712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                            CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N. meningitidis partial DNA sequence gnm_551 SEQ ID NO:551.
Pred. No. 1,2e-80;
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100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA82004 standard; DNA; 515 BP.
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                                   Conservative
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Rappuoli R, Pizza M;
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                   Best Local Similarity
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30-APR-1999;
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                                   Matches
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against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to a medicament) for treating, preventing or diagnosing infection due to be separable bacteria. For example, some of the identified proteins could be components of vaccines against Meningococus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences particularly organism-specific probes. Attempts to make efficacious Meningococus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have failed mainly due to antigen colerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface expended professionally variable or at least more conserved than other more variable regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACA
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                                                                                                                                                                                                                                                                                                                                                           29.0%; Score 290; DB 21;
100.0%; Pred. No. 1.2e-80;
tive 0; Mismatches 0;
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18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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25-MAY-2000; 2000US-207454P.
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                                                                                                                                                                                                                                                                                                                                                                                                      290; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV45308
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30-JUN-2000; 2000WO-US18061.

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        712 GGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 ATTANTGAATCGGCCAACGCGCGGGGGGGGGGTTTGCGTATTGGGCGCTCTTCCGCTT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTGTTATCCGCTCACAATTCCACACA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                   in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung tumour protein related nucleotide sequence SEQ ID NO:639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             952 CCTCGCTCACTGCTCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 cercecreacreacrescrescrescrescrescrescresces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 290; DB 23; Length 561; 100.0%; Pred. No. 1.1e-80; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 561 BP; 126 A; 146 C; 159 G; 130 T; 0 other;
                                                                                                                                                        Claim 1; Page 8966; 11750pp; English.
    Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF68704 standard; cDNA; 584 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0 Matches 290; Conservative
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Schlegel R, Endege WO,
                                      WPI; 2001-662795/76.
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The present invention describes immunogenic portions of lung tumourassociated proteins (I) and the nucleic acids (NAs) that encode them.

(I) have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumourassociated to proteins they encode may be used in the prevention, treatment and proteins they encode may be used in the prevention, treatment and cangodists of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to creat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (I). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NAs may be used to produce the lung-tumour associated protein according to standard recombinant DNA methodology. Conversely, antisense NA molecules may be administered to down regulate protein expression by and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in cancer. The (I) may be used as antigens in the production of antibodies and in assays to identify modulators (agoniets and antagonists) of the expression and activity of the protein. APF80803 to AAP58819 and AAB76818 represent human lung tumour protein related necession and protein sequences which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 ATTAATGAATCGGCCAACGCGGGGGGGGGGGTTTGCGGTATTGGGCGCTCTTCCGCTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892 ATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor-associated proteins and the nucleic acids that encode them,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for preventing, diagnosing and treating lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                     Lodes MJ, Fanger GR, Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 584 BP; 142 A; 159 C; 153 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.0%; Score 290; DB 22; Best Local Similarity 100.0%; Pred. No. 1.1e-80; Matches 290; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 360; 436pp; English.
                                                             99US-0419356.
99US-0466867.
99US-0476300.
                                                                                                                                06-MAR-2000; 2000US-0519642.
22-MAR-2000; 2000US-0533077.
10-APR-2000; 2000US-0566055.
27-APR-2000; 2000US-0560405.
05-JUN-2000; 2000US-0589184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the present invention.
                                                                                                                                                                                                                                                                                                                   Wang T, Bangur CS, Lc
Retter MW, Mannion J;
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Best Local Similarity
                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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                                                                                    17-DEC-1999;
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CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGTGC
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                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                       ACA10944 standard; cDNA; 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-2000; 2000US-0736457.
                                                                                                                                                                                                                                                                                                    05-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWITZER A P. MCNEILL P D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLAPPER J D.
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FANGER G R.
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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Clapper JD;
                                                                                                                                                                                                                                                                      ACA10944;
832
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(MCNE/)
(CLAP/)
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(FANG/)
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                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                          ACA10944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for tremoving tumour cells from a biological sample. The polynucleotide is also useful as probe or parimer to detect the level of mRNA encoding a tumour protein This sequence encodes a lung tumour associated protein recein regeneric described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynuclectide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
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                                                                                                                                                                                        tumour; cancer; T cell; immune response stimulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 584 BP; 142 A; 159 C; 153 G; 130 T; 0 other;
                                                                                                                                                         cDNA encoding clone #26843 of lung tumour protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID No 639; 223pp; English.
                                                                BP.
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29-AUG-2000, 2000US-0651563.
08-SEP-2000, 2000US-0651325.
26-SEP-2000, 2000US-0671325.
30-OCT-2000, 2000US-0702705.
13-DEC-2000; 2000US-0702705.
                                                                ABK38615 standard; cDNA; 584
                                                                                                                                                                                                                                                                                                                                    10-JUL-2001; 2001WO-US22058
                                                                                                                           (first entry)
                                                                                                                                                                                                            cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
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Marnerakis M,
                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                             21-MAY-2002
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                                                                                              ABK38615;
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                                                 ABK38615
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The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence ($2) mentioned in periodication, complement of $1, sequences consisting of at least 20 specification, complement of $1, sequences consisting of at least 20 contiguous residues of $1, sequences that hybridise to $1, sequences $1 having 75%, preferably 90%, identity to $1, or degenerate variants of $1 having 75%, preferably 90%, identity to $1, or degenerate variants of $1 having at least 70% preferably 90%, identity to a sequence encoded by the polynucleotide, or sequences specification, a sequence encoded by the polynucleotide, or sequence of a cancer for sequence encoded by the polynucleotide, an expression control sequence, a host cell cransformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polypeptide, an expression control sequence, a host cell antigen-binding fragment) that specifically binds to the polypeptide, comprising the presence of a cancer in a patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to the polyment confitting and/or expanding T cells specific for a tumour protein (comprising T cells with
                                                                                      216
                                                                                                                                                                                      951
                                                                                                                                                                                                                                                                             276
891
                                                                                                                                                                                                                                                             Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer
                                                                                 157 carraarrecerrecercacrececerriceaereeeaaacerereceeeaa
                                                                                                                                                                                      892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCCGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lung neuroendocrine carcinoma library MLN1 cDNA, SEQ
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the polynuclectide, protein or antigen-presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4+ and/or CD8+ T cells isolated from a patient with the polynuclectide, protein or antigen presenting cells that express the polynuclectide, such that T cells proliferated T cells, and thus comparison to patient an effective amount of the proliferated T cells, and thus inhibiting the development of a cancer in the patient. The patient composition for complying the present and scales are useful in a composition for a patient (particularly lung cancer). The oligonuclectide is useful for determining the presence of a cancer in a patient. The protein and coligonuclectides are useful in pharmaceutical compositions, e.g. carriers. The polynuclectide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molectides for inhibiting expression of tumour polymerclectide is consecuted in the patient patient sequence is a cDNA (full length, extended or partial)

The present sequence is a cDNA (full length, extended or partial)

Considered from a library derived from lung tumour/cancer cells. The sequence data for this patent did not form patient control of the printed specification, but was obtained in electronic control of control of the printed specification, but was obtained in electronic control of control of the printed specification, but was obtained in electronic control of the printed specification, but was obtained in electronic control of the printed specification, but was obtained in electronic control of the printed specification, but was obtained in electronic control of the printed specification, but was obtained in electronic control of the printed specification, but was obtained in electronic control of the printed specification, but were obtained and electronic control of the printed specification, but so the control of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.0%; Score 290; DB 25; Length 584; Best Local Similarity 100.0%; Pred. No. 1.1e-80; Matches 290; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer; cytostatic; vaccine; gene therapy; cancer;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer therapyand diagnosis associated cDNA #622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 584 BP; 142 A; 159 C; 153 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html?DocId=20020197669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX99895 standard; cDNA; 584 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer.
                                                                                                                                                                                                                                                                                                                            Durham M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
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                                                                                                                                                                                                                                                                                                                          Johnson JC, Retter MW,
Bangur CS, Mcnabb A;
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29.0%; Score 290; DB 25; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.1e-80;
Matches 290; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 584 BP; 142 A; 159 C; 153 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynuclectide, useful for preparing a compositinhibiting development of cancer, e.g. lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 639; 82pp; English
                                                                                                                                                                                                                                                                                                                                 Watanabe Y,
Vedvick TS,
                       2000US-0546259
2000US-0560406
                                                                                                                                 2000US-0658824
                                                                                                                                                                             2000US-0677419.
2000US-0702705.
2000US-0736457.
                                                                                                                                                          000US-0671325
                                                                   2000US-0589184
                                                                                                                                                                                                                                              03-MAY-2001; 2001US-0849626
2000US-0533077
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Fanger GR,
                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                 Henderson RA,
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    22-MAR-2000;
                                                  27-APR-2000;
                                                                     05-JUN-2000;
                                                                                                                                                          26-SEP-2000;
                                                                                                                 29-AUG-2000;
                                                                                                                                   08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                          Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 832
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891 216 951 276

10-JUL-2001; 2001US-0902941.

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Method for determining open reading frames of the genome of an organism using primers at low stringency conditions, useful in the construction of contigs or constructs of sequenced nucleic acid molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a cDNA sequence obtained using a method for determining open reading frames (ORFS) of the genome of an organism. An aliquot of mRNA from human breast cancer cells was mixed with a single, arbitrary primer, Moloney murine leukaemia virus reverse transcriptase, reverse transcriptase buffer and GNTPs. The mixture was incubated under low stringency conditions to yield single stranded CDNA. The same primer was then used to amplify the CDNA by PCR. Rather than providing nucleotide sequence information from the non-coding the more interesting and relevant internal portions, such as ORFS. The method also permits the construction of contigs of sequenced nucleic
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            cDNA synthesis; contig sequence construction; low stringency; cDNA sequencing; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.0%; Score 290; DB 21; Length 598; 100.0%; Pred. No. 1.1e-80; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 598 BP; 136 A; 170 C; 155 G; 132 T; 5 other;
                                                                                                                                                                                                                                                                         Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 112; 113pp; English.
                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                       98US-0196716,
                                                                                                                                                                    99WO-US27430
                                                                                                                                                                                                                                                                           Dias Neto E,
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                Human; arbitrary primer;
open reading frame; ORF;
                                                                                                                                                                                                                                                                                                          WPI; 2000-400100/34.
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Matches 290; Conserv
                                                                                                   WO200031299-A2
                                                                    Homo sapiens
                                                                                                                                                                      19-NOV-1999;
                                                                                                                                                                                                         20-NOV-1998;
                                                                                                                                    02-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frames (ORPS) of the genome of an organism comprising contacting messenger RNA from a cell of the organism with a single, oligonucleotide primer at low stringency. The method is an improved ORESTS sequencing method. The methods of the present invention are useful for sequencing of, essentially, the entire coding component of an organism, identification of previously unknown nucleic acid molecules, assigning previously identified nucleotide sequences to internal regions of genes and population studies that identify genes associated with diseases such as heart diseases, bronchitle, Alzheimer's disease, autoimmune diseases and congenital diseases. This polynucleotide represents a DNA sequence that is used in the novel method of the invention.
                                          Open reading frame; ORF; low stringency; sequencing; ORESTES; bronchitis; identification; internal region; population study; heart disease; Alzheimer's disease; autoimmune disease; congenital disease; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 ATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                        Determining ORFs of the genome by contacting mRNA with a single oligonucleotide primer, useful for population studies that identify genes associated with diseases such as cardiovascular, autoimmune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for determining open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 598 BP; 136 A; 170 C; 155 G; 132 T; 5 other;
            Orestes sequencing method related DNA SEQ ID No 387.
                                                                                                                                                                                                                                                                                                                         Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 161-162; 166pp; English
                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                       07-NOV-2000; 2000US-246313P.
                                                                                                                                                                                                                        01-NOV-2001; 2001WO-US46665.
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Matches 290; Conservative
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                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-750567/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   congenital diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                     WO200274994-A2
                                                                                                                                                                                                                                                                                                                             Simpson AJG,
                                                                                                                    Homo sapiens
                                                                                                                                                                                      26-SEP-2002
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129 891 189 951 249

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Search completed: February 15, 2004, 22:40:26 Job time : 327.065 secs

(first entry)

02-JAN-2003

ABT12681;

ABT12681 standard;

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Sequence 1, Appli
Sequence 2, Appli
Sequence 639, App
Sequence 639, App
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
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26, Appl
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                                                                                    February 15, 2004, 10:22:55; search time 73.6147 Seconds (without alignments) 6001.851 Million cell updates/sec
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(cgn2 6/ptodata/2/ina/5A COMB.seq:*
(cgn2 6/ptodata/2/ina/5B_COMB.seq:*
(cgn2 6/ptodata/2/ina/6A_COMB.seq:*
(cgn2 6/ptodata/2/ina/6B_COMB.seq:*
(cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
(cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
(cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-475C-259
US-09-328-475C-195
US-09-328-475C-195
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US-09-702-705-639
US-09-736-457-639
US-08-706-724
US-08-706-706-26
US-08-706-706-26
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US-08-706-702-25
US-08-706-702-25
US-08-706-702-25
US-09-238-46-28-3
US-09-272-103-3
US-09-272-103-3
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                                                                                                                                                US-09-921-143-36_COPY_2000_3000
                                                                                                                                                                                                                                                     569978 segs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                        - nucleic search, using sw model
                                                                                                                                                                                                         OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                               Perfect score:
                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                    Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                      Searched:
                                                                                      Run on:
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RESULT 1
US-08-155-888-1
US-08-155-888-1
Sequence 1, Application US/08155888
Sedemore 1, Application US/08155888
Sedemore 1, Application US/08155888
Sedemore 1, Application
Sedemore 1, Sedemore 1, Sedemore 2, Applicant: Bedstrom, Richard C.
APPLICANT: Bedstrom, Richard C.
APPLICANT: Bedstrom, DELIVERING POLYNUCLEOTIDE VACCINE PROTECTIVE
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
UNDERSPONDENCES. 2
CORRESPONDENCES. 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical Res. & Dev. Cmd.
STREET: Bldd 1, T-12 8901 Wisconsin Ave.
CITY: Betheeda
CITY: Maryland
                                                                                          Sequence 17, Appl
Sequence 11, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 21, Appli
Sequence 9, Appendix Sequence 7, Appendix Bequence 17, Appendix Bequence 17, Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
LOCATION: 1..755
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="promoter"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /label=CMV-IE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFPLICATION NUMBER: US/US/155,083
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGBAT INFORMATION:
NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C. 75,851
FELEPHONE: (202) 295-6759
TELEPAN: (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
     NAME/KEY: promoter
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2759 CTTGTCTCACAGCCATGCAACCCTTGCCTCTGTGCTGACTTAGCAGGGGATAAAGTGAG 2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2939 chachdaadchdaadadccadaddaccadhaacchraahcchradachchdaadahd 2998
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NAME/KEY: CDS

LOCATION: 933.2367

LOCATION: 933.2367

LOCATION: 933.2367

LOCATION: 933.2367

COTHER INFORMATION: /function= 'protein' protective against malaria"

OTHER INFORMATION: /function= 'protein'
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OTHER INFORMATION: /label= IL2-CSP

OTHER INFORMATION: /label= IL2-CSP

OTHER INFORMATION: /citation= ([1])
PUBLICATION INFORMATION: /citation= ([1])
AUTHORS: Bedgath, Match
AUTHORS: Bedgath, Match
AUTHORS: Hedgtrom, Richard C.
AUTHORS: Hedgtrom, Richard C.
AUTHORS: Hedgtrom, with Plasmodium yoelii CS protein
TITLE: Vaccination with Plasmodium yoelii cs protein
TITLE: plasmid DNA protects against malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 GAGGGATGGTAACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 CTTGTCTCACAGCCATGCAACCCTTGCCTCTGTGCTGACTTAGCAGGGGATAAAGTGAG 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 CAACTGGAGCTGGAGGCCCGGGGGCAGGTGACCTTCAGACCTTGGCCACTGGAGGTG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 CTGGAGAACTACTGCAACTAGGCCCACCACTACCCTGTCCACCCCCTCTGCAATGAATAAA 590
/note= "This feature acts as a promoter for any
downstream DNA sequence."
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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30.7%; Score 307; DB 3; Length 55;
Best Local Similarity 99.3%; Pred. No. 1.9e-112;
Matches 457; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
AUTHORS: Cullen, Bryan R.
TITLE: TRANS-ACTIVATION OF HUMAN IMMUNODEFICIENCY
TITLE: VIRUS OCCURS VIA A BIMODAL MECHANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATE: 26 SEP-1986
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4732
OTHER INFORMATION:
OTHER INFORMATION:
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US-09-486-336A-2
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; Sequence 2, Application US/09486336A; Patent No. 6566336

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712 CGIAAICAIGGICAIAGCIGITICCIGIGAAAIIGIIAICCGCICACAAIICCACACA 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            832 CATTAATTGCGTTGCGCTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                             APPLICANT: SAITO, ISA

TITLE OF INVENTION: A COMPOUND TO ALKYLATE FOR THE SPECIFIC
TITLE OF INVENTION: SEQUENCE IN DNA AND ITS METHOD OF PREPARATION
TITLE OF INVENTION: SEQUENCE IN DNA AND ITS METHOD OF PREPARATION
FILE REPERENCE: 49430 (71526)
CURRENT APPLICATION NUMBER: US/09/486,336A
CURRENT PILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: POT/JP99/01228
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FREESEQ FOR Windows Version 3.0
SEQ ID NO 2
LENGTH: 450
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APPLICANT: Rannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE TELE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 ceredeneacredenedenedenedredenedenedesedadesena 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 290; DB 4; Length 450; 100.0%; Pred. No. 1.6e-105; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vadvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: SUGIYAMA, Hiroshi
APPLICANT: TAO, Zhi Fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 290; Conservative
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US-09-702-705-639
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SOFTWARE: FastSEQ for
SEQ ID NO 639
LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: pUC 18
US-09-486-336A-2
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US-09-702-705-639
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952 CCTCGCTCACTGACTCGCTGGCTCGTTCGGCTGCGGCGAGCGGTA 1001
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2800006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 701 base pairs
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EDNESS: both
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                                                                                                         RESULT 5
US-08-706-702-24
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                                                                                    712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA 771
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                                                                                                                                                                        0; Gaps
                                                 0; Gaps
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILICATION DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.0%; Score 290; DB 4; Length 584; Best Local Similarity 100.0%; Pred. No. 1.5e-105; Matches 290; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.5e~105;
iive 0; Mismatches 0;
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Patent No. 6509448
GENERAL INFORMATION:
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Bangur, Chaitanya S.
Lodes, Michael A.
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Best Local Similarity 100.03
Matches 290; Conservative
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Vedvick, Tom
Carter, Darrick
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Mannion, Jane
Fan, Ligun
Wang, Aijun
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US-09-736-457-639
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SEQ ID NO 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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277 CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCTGCGCGGAGCGGTA 326
                                                                                                                                                                  Generoe 24, Application US/08706702
| Ratent No. 5948614
| GENERAL INFORMATION:
| TITLE PROMATION:
| TITLE OF INVENTION: maritima and Mutants Thereof
| TITLE OF INVENTION: maritima and Mutants Thereof
| NUMBER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS:
| ADDRESSE: STENNS, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 701;
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29.0%; Score 290; DB 2; Length 701
Best Local Similarity 100.0%; Pred. No. 1.5e-105;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/706,702
PILING DATE: 04-ANG-1996
PILING DATE: 14-ANG-1996
PILING DATE: 14-ANG-1996
PILING DATE: 14-ANG-1996
PILING DATE: 02-OCT-1995
PILING DATE: 02-OCT-1995
PILING DATE: 02-OCT-1995
PILING DATE: 02-OCT-1995
PILING APPLICATION DATA:
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US-08-706-706-24
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                                   892 ATTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
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                                                                                                                                                                                                                                                                                          952 CCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGCGAGCGGTA 1001
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Batent No. 6015668
GENERAL INFORMATION:
APPLICANT: Hughes, A. John
APPLICANT: Chatteriee, Deb K.
TITLE OF INVENTION:
Cloned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: Hadhington
CLTY: Washington
                                                                                                                                                                                                                                                                                                                                                              COUNTY: UGA

ZIP: 20005-3934

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/08/706,706
FILING DATE: 06-SEP-1996
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-OCT-1995
FRICK APPLICATION NUMBER: US 08/537,400
FILING DATE: 01-JAN-1995
FRICK APPLICATION NUMBER: US 08/537,400
FILING DATE: 01-JAN-1995
FRICK APPLICATION NUMBER: US 08/37,400
FILING DATE: 01-JAN-1995
FRICK APPLICATION NUMBER: US 08/37,400
FILING DATE: 01-JAN-1995
FRICK APPLICATION NUMBER: US 08/37,337
FILING DATE: 10-JAN-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 11-DEC-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/537,337
FILING DATE: 11-DEC-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/537,337
FILING DATE: 01-DEC-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/525,057
FRICK APPLICATION DATA:
APPLICATION DATA
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REGISTRATION NUMBER: 32,893
REFERENCE/FOCKET NUMBER: 094
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 24:
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LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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US-08-706-706-24
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Patent No. 6506560

GENERAL INFORMATION:

APPLICANT: Hughes, A. John

Chatterjee, Deb K.

TILLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and
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CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: USA
Query Match 29.0%; Score 290; DB 3; Length 701; Best Local Similarity 100.0%; Pred. No. 1.5e-105; Matches 290; Conservative 0; Mismatches 0; Indels
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MEDIUM TYCE: RIOPPY disk
COMPUTER: INDAPY COMPALIALE
COMPUTER: INDAPPE COMPALIALE
APPLICATION NUMBER: US/08/238,471
FILING DATE: 28-Jan-1999
FRIOR APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
APPLICATION NUMBER: US/08/537,400
FILING DATE: 01-JAN-1995
APPLICATION NUMBER: US/08/370,190
FILING DATE: US/08/370,190
FILING DATE: US/08/370,190
FILING DATE: US/08/370,190
FILING DATE: US/08/370,190
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APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/537,397
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US 08/537,397

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APPLICATION NUMBER:
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Patent No. 5548614
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Maritima and Mutants Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STERRET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                          Query Match 29.0%; Score 290; DB 4; Length 701; Best Local Similarity 100.0%; Pred. No. 1.5e-105; Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUNTRY: USA

COMPUTER: DC

CONTRY: USA

ZIP: DC

ZIP: DC

ZIP: CONSTRY: USA

ZIP: SEADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERAITMG SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,702

FILING DATE: 06-8EP-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/689,807

FILING DATE: 14-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                          TOPOLOGY: both

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-238-471-24
TELECOMMUNICATION INFORMATION:
                TELEPRONE: 202-371-260
INFORMATION FOR SEQ 1D NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-706-702-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 ATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gabs
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Patent No. 6015668

GENERAL INFORMATION:
APPLICANT: Hughes, A. John
APPLICANT: Clanterfiee, Deb K.
TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES: 26
CORRESPENDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STRRET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 CCTCGCTCACTGGCTGCGCTCGGTCGTTCGGCTGCGGCGGCGAGCGGTA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
29.0%; Score 290; DB 2; Length 71.
Best Local Similarity 100.0%; Pred. No. 1.4e-105;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: ILEM FC compatible
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/689,807
                                                                                                                                    NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERNICE/DOCKET NUMBER: 0942.2800006
TELECOMMINICATION INFORMATION:
TELEPHONE: 202-371-260
                                                         US 08/525,057
                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
US-08-706-702-26
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                : 713 base pairs
nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-706-706-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTAATTGCGCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.0%; Score 290; DB 3; Length 713; Best Local Similarity 100.0%; Pred. No. 1.4e-105; Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   0942.2800005
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 713 base pairs TYPE: mucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                     202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 ATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.0%; Score 290; DB 4; Length 713; Best Local Similarity 100.0%; Pred. No. 1.4e-105; Matches 290; Conservative 0; Mismatches 0; Indels
                                   COMPUTER FEADABLE FORM:

MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,471
FILING DATE: 28-A2n-1999
CLASSIFICATION PATA:
PRIOR APPLICATION PATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-07-1995
FILING DATE: 02-07-1995
FILING DATE: US 08/370,190
FILING DATE: US 08/370,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-5EP-1994
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-007-1995
APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-58P-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
SRQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-238-471-26
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RESULT 11 US-08-998-416-55

Sequence 26, Application US/09238471
| Patent No. 6506560
| GENERAL INFORMATION:
| APPLICANT: Hughes, A. John |
| TITLE OF INVENTION: Claned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS: 8
| ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600 CITY: Washington

US-09-238-471-26

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TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-706-702-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                   RESULT 12
US-08-706-702-25
                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGGTCACAATTCCACACA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 CGTAATCATGGTCATAGCTGTTTCCTGTGAAAATTGTTATCCGCTCACAATTCCACACA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
Sequence 55, Application US/08998416
Patent No. 6239264
Patent No. 6239264
Patent No. 6239264

Patent No. 6239264

APPLICANT: Philippsen, Peter
APPLICANT: Stainer, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischule, Philipp
APPLICANT: Rebischule, Philipp
APPLICANT: Nebischule, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              952 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
29.0%; Score 290; DB 3; Length 716
Best Local Similarity 100.0%; Pred. No. 1.4e-105;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: No. 623264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/NS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION NUMBER: US/08/998,416
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: GROWN:
APPLICATION NUMBER: GROWN:
APPLICATION NUMBER: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Med-98, J. Timothy
REGRENCE/DOCKET NUMBER: 38/241
REFERENCE/DOCKET NUMBER: 38/241
REFERENCE/DOCKET NUMBER: 38/241
REFERENCE/DOCKET NUMBER: 39/241-8689
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LEMMOTH. 716 APS TAILS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: PAGI015UP
US-08-998-416-55
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Sequence 25, Application US/08706702
Patent No. 5948614
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Maritima and Mutants Thereof
NUMBER OF SEQUENCES 26
CORRESPONDENCE ADDRESS:
ADDRESSES STRENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET 1100 New York Ave., N.W., Suite 600
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.0%; Score 290; DB 2; Length 717; Best Local Similarity 100.0%; Pred. No. 1.4e-105; Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 20005-3934

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM;

MEDIOW TYPE: Floppy disk

COMPUTER: IBM PC compatible

CORPTURE: IBM PC compatible

CORPTURE: Batenin Release #1.0, Version #1.30

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/706,702

FILING DATE: 06-SEP-1996

CLASSIFICATION NUMBER: US 08/689,807

FILING DATE: 14-AUG.-1996

PRIOR APPLICATION NUMBER: US 08/537,400

FILING DATE: US-02-02T-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/537,599

FILING DATE: US-02-02T-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/537,397

FILING DATE: US-02-02T-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/525,057

FILING DATE: US-02-02T-1995

PRIOR APPLICATION DATA:

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REGISTRATION NUMBER: 32,893
REFERENCE, DOCKET NUMBER: 0942.2800006
TELECOMMULICATION INFORMATION:
TELEFHONE: 202-371-2600
TELEFAX: 202-371-2540
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                             265 ATTAATGAATCGGCCAACGCGCGGGGAGCGGTTTGCGTTTGCGTTTGGGCGTTTTGCGTTTTCCGCTTT 324
892 ATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
                                                                                     952 CCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
                                                                                                                                                                                                                                     Sequence 25, Application US/08706706

Patent NO. 6015668

GENERAL INFORMATION:
APPLICANT: Hughes, A. John
APPLICANT: Chatteriee, Deb K.
TILLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES. 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STRRET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
                                                                                                             325 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
A PPPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
CLASSIPTCATION 435
PRIOR APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0942.2800005
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PRIOR DATE: 01-JAN-1995

PRIOR DATE: 01-JAN-1995

PRIOR PEPLICATION DATE: 08/316,423

PILING DATE: 30-SEP-1994

PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/576,759

PILING DATE: 21-DEC-1995

PRIOR APPLICATION NUMBER: US 08/577,397

FILING DATE: 02-OCT-1995

PRIOR APPLICATION NUMBER: US 08/537,397

FILING DATE: 02-OCT-1995

PRIOR APPLICATION NUMBER: US 08/525,057

FILING DATE: 08-SEP-1995

ATTORNEY AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/537,400 FILING DATE: 02-OCT-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 25:
SEGUENCE CHARACTERISTICS:
LENGTH: 717 base, pairs
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E: DNA (genomic)
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ZIP: 20005-3934
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE:
US-08-706-706-25
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STATE: D
COUNTRY:
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29.0%; Score 290; DB 3; Length 717;

Query Match

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85 céraarcardercaraccierricerereraaarrerraeceercacaarrecada 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 ATTAATGAATCGGCCAACGCGCGGGAAGGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 324
                                                                                       712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                0; Gaps
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Sequence 25, Application US/09238471
Sequence 25, Application US/09238471
Sequence 25, Application US/09238471
GENERAL INFORMATION:
TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES: 26
CORRESPONDENCE 26
CORRESPONDENCE AMOUNT VECTRE GOLDSTEIN & FOX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 952 CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 1001
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ilarity 100.0%; Pred. No. 1.4e-105; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/08/706,706
FILING DATE: 06.5EP-1996
APPLICATION NUMBER: US/08/706,706
FILING DATE: 14-AUG-1996
APPLICATION NUMBER: US/08/537,400
FILING DATE: 02-OCT-1995
APPLICATION NUMBER: US/08/370,190
FILING DATE: 01-JAN-1995
APPLICATION NUMBER: US/08/370,190
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: US/08/376,759
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: US/08/376,759
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APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-CT-1995
APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-Jan-1999
CLASSIFICATION: <Unknown>
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Best Local Similarity
Matches 290; Conserv
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712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTGTTATCCGCTCACAATTCCACACA 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 CATTAATTGCGTTGCCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ATTAATGAATCGGCCAACGCGCGGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 324
                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                            Length 717;
                                                                                                                                                                                                                                                          Query Match 29.0%; Score 290; DB 4; Length 717 Best Local Similarity 100.0%; Pred. No. 1.4e-105; Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08726462B
Sequence 3, Application US/08726462B
Patent No. 580096
GENERAL INFORMATION:
PERKIN-Elmer Corporation, Applied Biosystems APPLICANT: Division
TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED TITLE OF INVENTION: FUUORESCENCE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
ADDRESSEE: & Rosati
STREET: 650 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 34304-1050
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM compatible
OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
SOTTWARE: MORGHERET (DOS) TEXT format
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,462B
// INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
MOLECULE TYPE: DAN (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-238-471-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,330
FILING DATE: May 3, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,196
FILING DATE: June 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: David J. Weitz
REGISTRATION NUMBER: 38,362
REFERENCE/DOCKET NUMBER: PELM4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
COUNTRY: USA
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US-08-726-462B-3
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832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGTGC 891
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                                                                                                                                                                                                                                                                                                                                                                                                   712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA 771
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                                                                                                                                                                                                                                                                                         Query Match 29.0%; Score 290; DB 1; Length 738; Best Local Similarity 100.0%; Pred. No. 1.4e-105; Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 15, 2004, 19:10:14 Job time : 75.6147 secs
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 493-6810
TELEPHONE: (415) 493-6811
INFORMATION FOR SEQ ID NO: 3;
SEQUENCE CHARACTERISTICS;
LENGTH: 738 nucleictides
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: linear
US-08-726-4628-3
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Sequence 3110, Ap
Sequence 103, App
Sequence 3746, Ap
Sequence 3746, Ap
Sequence 3746, Ap
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3746, Ap
3746, Ap
639, App
639, App
639, App
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                                                                                                                February 15, 2004, 16:21:35 ; Search time 420.484 Seconds (without alignments) 8769.219 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2. (cgn2_6)ptodata/1/pubpna/US07_PUBCOMB seq:*

3. (cgn2_6)ptodata/1/pubpna/US07_BW_PUB.seq:*

3. (cgn2_6)ptodata/1/pubpna/US06_FUBCOMB.seq:*

3. (cgn2_6)ptodata/1/pubpna/US06_FUBCOMB.seq:*

3. (cgn2_6)ptodata/1/pubpna/DSOF_NEW_PUB.seq:*

3. (cgn2_6)ptodata/1/pubpna/DSOF_NEW_PUB.seq:*

3. (cgn2_6)ptodata/1/pubpna/US08_FUBCOMB.seq:*

3. (cgn2_6)ptodata/1/pubpna/US08_PUBCOMB.seq:*

3. (cgn2_6)ptodata/1/pubpna/US08_FUBCOMB.seq:*

3. (cgn2_6)ptodata/1/pubpna/US09_FUBCOMB.seq:*

4. (cgn2_6)ptodata/1/pubpna/US00_NEW_PUB.seq:*

4. (cgn2_6)ptodata/1/pubpna/US00_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-067-4758-3110
US-10-09-796-692-3746
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                                                                                                                                                                                                                                                                                                                                            2449703 seqs, 1841816367 residues
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                                                                     OM nucleic - nucleic search, using sw model
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Sequence 17, Appl Sequence 259, App Sequence 259, App Sequence 195, App Sequence 70, Appl Sequence 182, App Sequence 181, App Sequence 482, App Sequence 404, App Sequence 165, App Sequence 273, Appli Sequence 3, Appli Sequence 350, Appli
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                                                           Sequence 18505, A
Sequence 1382, Ap
Sequence 9687, Ap
Sequence 971, Ap
Sequence 24, Appl
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Publication No. US20030215921A1

FURRRAL INFORMATION:

APPLICANT: Coleman, Timothy

TITLE OF INVENTION: Vascular Endothelial Growth Factor-2

FILE REPERENCE: PF112P6

CURRENT APPLICATION NUMBER: US/09/921,143

CURRENT FILING DATE: 2001-08-03

FRIOR PLING DATE: 2001-08-03

FRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.0
3 US-10-113-872-639

5 US-09-764-863-18505

0 US-09-764-891-8687

1 US-09-764-891-9113

1 US-09-764-891-9113

1 US-09-764-891-9113

1 US-09-764-891-9113

1 US-09-229-173-25

1 US-09-229-173-25

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1 US-10-289-696-25

1 US-10-289-696-25

1 US-10-289-696-26

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1 US-10-202-193-195

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US-09-764-83-404
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2 US-10-125-540-182
5 US-10-125-540-182
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LENGTH: 5283
TYPE: DNA
ORGANISM: homo sapiens
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US-09-921-143-36
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US-09-921-143-36
             Query Match
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2060 AGCTGCCAGGAAGAAGTGAGAATCCTTCCTTAAGTCTCCTAGGTGACGGGGGGGCTAG 2119

61 AGCTGCCAGGAAGGAGTGAGAATCCTTTCCTTAAGTCTCCTTAGGTGGTGGTGACGGGTGGCTAG 120

셤 8

Sequence

Seguence Sequence

181 AACAGGATGTGTAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCAC 240

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TOGGCCAACGCGCGGGGGGGGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCA 950
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2180 AACAGGATGTGTAAGGTTTTGGAGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCAC 2239
                                                   2300 GGCTAATCAGGGGGTCGCTCAGCTCCTAACTGGATTGTCCTATGTGTCTTTGCTTCT 2359
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                                                                                                                                                           361 GTGCTGCTGATGCTCTGCCCTGTGTGACATGACCTCCCTGGCAGTGGCACAACTGGAGC 420
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                                                                                                                                                                                                                                                                                      241 AGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAAAAGCCTG 300
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GURREAL INTORMATION:
APPLICANT: Algaete, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER.
TITLE OF INVENTION: CAMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER.
TITLE OF INVENTION: CAMPOSITION AND THE STORE APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-22
PRIOR FILING DATE: 2000-04-22
PRIOR PELING DATE: 2000-04-22
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/202,994
PRIOR APPLICATION NUMBER: 60/202,994
PRIOR PLING DATE: 2000-05-02
PRIOR PLING DATE: 2000-05-02
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-06-04

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                                                                                                                                                                                            ; FEATURE:
; OTHERNATION: Baculovirus transfer vector pVL1393
US-10-394-511-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3110, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 9632
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-796-692-3110
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retreer, Marc W.
APPLICANT: Composition and Methods for the Detection, Diagnosis and Thera
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and TILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and TILE OF INVENTION: Hematological Malignancies
FILIE OF INVENTION: Hematological Malignancies
CURRENT PELING DATE: 2000-03-13
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-04
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                                                                                                                                                                                                                       Query Match
29.0%; Score 290; DB 12; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps
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ORGANISM: Homo sapiens
                                                                                                                  : Homo sapiens
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US-10-154-884B-3110
    ; SEQ ID NO 3110
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LENGTH: 380
                                                                               TYPE: DNA ORGANISM: 1
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Carter, Lausen
APPLICANT: Carter, Lausen
APPLICANT: Carter, Lausen
APPLICANT: Cortixa Corporation
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APPLICANT: Cortixa Corporation
APPLICANT: Movill, Faratiological Malignancies
FILE REPERROIC 2014082 01460208
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US 60/186,126
FRIOR APPLICATION NUMBER: US 60/186,126
FRIOR APPLICATION NUMBER: US 60/186,126
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR FILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-22
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-24
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-24
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-24
FRIOR APPLICATION NUMBER: US 60/200,203
FRIOR FILING DATE: 2000-05-24
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FRIOR FILING DATE: 2000-05-24
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR FILING DATE: 2000-05-24
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29.0%; Score 290; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps
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                                                                      TYPE: DNA
CRGANISM: Homo sapiens
US-09-796-692-3110
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APPLICANT: Chao, Qimin APPLICANT: Chao, Liuigh APPLICANT: Chao, Liuigh APPLICANT: Carssoo, Liuigh M. APPLICANT: Sass, Philip M. APPLICANT: Nicolaides, Nicholas C. TITLE OF INVERTION Genetic Hyperamutability of Plants for Gene Discovery and Diagno TILE REFERENCE: AG0002018 (MOR-0133) CURRENT FILING DATE: 2002-10-11 CURRENT FILING DATE: 2002-10-11 PRIOR FILING DATE: 2001-10-12 NUMBER OF SEQ ID NOS: 129 SOSTWARE: Patentin version 3.1 SEQ ID NO 103
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                                                                                             Length 380;
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29.0%; Score 290; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0;
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Conservative 0; Mismatches
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   , ORGANISM: Homo sapiens
US-10-040-862-3110
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APPLICANT: Algate, Faul A.
APPLICANT: Algate, Faul A.
APPLICANT: Mannion, Jame
APPLICANT: Retrier, Marc
TILLE OF INVENTION: Lompositions and Methods for the Detection, Diagnosis and Therapy
FILE DE INVENTION: Hematological Malignancies
FILE STERNENCE: 014058-01522003
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PELICATION NUMBER: US 60/200,549
PRIOR PELICATION NUMBER: US 60/200,549
PRIOR PELICATION NUMBER: US 60/202,044
PRIOR PELICATION NUMBER: US 60/202,044
PRIOR PELICATION NUMBER: US 60/202,446
PRIOR PELICATION NUMBER: US 60/202,416
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PRIOR PELICATION US 60/200,600
PRIOR PELICATION US 60/2
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                                                        Query Match 29.0%; Score 290; DB 12; Length 380; Best Local Similarity 100.0%; Pred. No. 1.2e-143; Matches 290; Conservative 0; Mismatches 0; Indels (
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Sequence 3110, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
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US-10-154-884B-3110
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APPLICANT: Algate, Paul. And Application of Applicant: Algate, Paul. Applicant: Algate, Paul. Applicant: Algate, Paul. Applicant: Clapper, Jonachan David Applicant: Clapper, Jonachan David Applicant: Clapper, Jonachan David Applicant: Carter Lauren Applicant: Carter Lauren Applicant: Carter Lauren Applicant: Carter Lauren Applicant: Corixa Corporation and Methods for the Detection, Diagnosis and Theritile Delivers: Colixa Corporation and Methods for the Detection, Diagnosis and Theritile Delivers: Colixa Corporation and Methods for the Detection, Diagnosis and Theritile Delivers: 2002-01-22 CURRENT FILING DATE: 2000-03-01 CORPORATION NUMBER: US 60/186,126 PRIOR PELICATION NUMBER: US 60/186,126 PRIOR PELICATION NUMBER: US 60/200,545 PRIOR PILING DATE: 2000-04-22 PRIOR PILING DATE: 2000-05-01 PRIOR PILING DATE: 2000-05-01 PRIOR PILING DATE: 2000-05-01 PRIOR PAPLICATION NUMBER: US 60/200,303 PRIOR PILING DATE: 2000-05-01 PRIOR PAPLICATION NUMBER: US 60/200,004 PRIOR APPLICATION NUMBER: US 60/200,004 PRIOR APPLICATION NUMBER: US 60/200,004 PRIOR PILING DATE: 2000-05-01 PRIO
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249 CCTCGCTCACTGACTGGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.0%; Score 290; DB 12; L 100.0%; Pred. No. 1.2e-143; tive 0; Mismatches 0;
                                                                                                                                                                                                             Sequence 3746, Application US/10057475B Publication No. US20040002068A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(557)

; OTHER INFORMATION: n = g, a, c or t

US-10-057-475B-3746
                                                                                                                                                                                                                                                                                                                             APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathar
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Best Local Similarity 100.
Matches 290; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAATTCCACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTAATGAATCGGCCAACGCGCGGAGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
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       323 CCTCGCTCACTGACTCGCTGCGCTCGGTCGCTTCGGCTGCGGCGAGCGGTA 372
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29.0%; Score 290; DB 10; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TILLE REFERENCE: 2007-03-01
PRIOR PLILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2000-08-07
PRIOR PRI
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US-09-796-692-3746
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LOCATION: (504)
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APPLICANT: Reter, Mannen, Jame
APPLICANT: Reter, Marc
APPLICANT: Reter, Marc
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther:
ITILE OF INVENTION: Hemacological Malignancies
CURRENT FILING DATE: 2001-11-06
FRICE REPRENCE: 101406-2018-2006
FRICE REPRENCE: 101406-2018-2006
FRICE REPRENCE: 101406-2018-2006
FRICE REPRENCE: 101406-2018-2006
FRICE RETURNG DATE: 2000-04-20
FRICE RELING DATE: 2000-06-20
FRICE RELING DATE: 2000-06-30
FRICE RELING DATE: 2000
189 ATTAATGAGCCAACGCGCGGGGGAGAGGGGGTTTGCGTATTGGGGCGCTCTTCCGCTT 248
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                                                                                                               952 CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 1001
                                                                                                                                                                249 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGCTA 298
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29.0%; Score 290; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                Sequence 3746, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
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COCATION: (504)
COTHER INFORMATION: n=A,T,C or G
US-10-040-862-3746
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-040-862-3746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ## APPLICANT: Galger, Alexander
## APPLICANT: Galger, Alexander
## APPLICANT: Galger, Alexander
## APPLICANT: Galger, Alexander
## APPLICANT: Retter, Marc W.
## APPLICANT: Corixa Corporation
## APPLICANT: Corixa Corporation
## APPLICANT: Corixa Corpositions and Methods for the Detection, Diagnosis and Therapy
## TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
## TITLE OF INVENTION: Hematological Malignancies
## TITLE OF INVENTION: OHISER: US 60/186,126
## RIOR PELICATION WUMBER: US 60/180,479
## RIOR PELICATION NUMBER: US 60/190,479
## RIOR PELICATION NUMBER: US 60/200,793
## RIOR APPLICATION NUMBER: US 60/200,793
## RIOR PELICATION NUMBER: US 60/200,793
## REAL PELICATION NUMBER: US 60/
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; LOCATION: (1)...(557)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-3746
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Best Local Similarity 100.
Matches 290; Conservative
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ORGANISM: Homo sapiens
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US-10-154-884B-3746
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Watanabe, Yoshihiro
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LENGIH: 584
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                                                                                        189 ATTAATGAATCGGCCAACGCGGGGAGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
   CATTAATTGCGTTGCGCTCACTGCCCGC
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No. US20020168637A1
                                                                                                                                                                                                                                                                          Wang, Tongtong
Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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APPLICANT: Wang, Aijun
TITLE OF INVENTION: CON
TITLE OF INVENTION: DIR
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ORGANISM: Homo sapien
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US-09-736-457-639
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ENGTH: 584
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APPLICANT: Bangur. Gary
APPLICANT: Fanger. Gary
APPLICANT: Warg, Aijun
APPLICANT: Warg, Tongtong
APPLICANT: Warg, Tongtong
APPLICANT: Wordell, Patricia
APPLICANT: Clapper. Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 639
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APPLICANT: Marrerak, Margarita
APPLICANT: Marrerak, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Thomas S.
APPLICANT: Penger, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Mandab, Andria
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.12.478617
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001.07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020197669A1
GENERAL INFORMATION:
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CRCANISM: Homo sapiens
US-09-902-941-639
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ORGANISM: Homo sapien
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FULLICATION NO. US20030125245A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DAGNOSIT ON FOUR CANCER.
FILE REFERENCE: 210121.478G3
CURRENT TAILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 785
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 639
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29.0%; Score 290; DB 11; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels
                    0; Indels
Best Local Similarity 100.0%; Pred. No. 1.2e-143; Matches 290; Conservative 0; Mismatches 0;
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, ORGANISM: Homo sapien
US-09-476-300-639
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US-09-476-300-639
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BF361564 pot 17-64
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AZ254213 a GF0612.x
AZ254213 a GF0613 b BF193803 d Ge33510.x
BF93803 d Ge35510.x
BF93803 d Ge35510.x
BF93803 d Ge35510.x
BF93834 d Ge41511.x
BF93834 d Ge41511.x
BF93834 d Ge3610.x
BF938603 d Ge3610.x
BF938603 d Ge3610.x
BF938610 d Ge3600.x
BF938610
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B1940910.1 G1:16255382
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B1937979 de29e08.x
CB859029 H109B01w
B82861 RPCII1-18D2
AL475038 T. brucei
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WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Feax: 314 286 1800
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Xenopus laevis
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B1675829 dag61e05.
B1937546 dd92b12.y
AU224539 AU224539
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                    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Gapop_60.0 , Gapext 60.0
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gb_gss2: *
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WashU Xenopus EST project, 1999
WashIUX Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Bmail: est@watson.wustl.edu
Library constructed by N. Garrett, E. ellefroid, and A.M. Zorn
(Wellcome/CRC Institute). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Conscrtium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stops: 273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
/mol_type="mRNA"
/dolone="mRNA"
/dolone="mRNA"
/dolone="mRNA"
/dolone="mRNA"
/dolone="mRNA"
/dolone="mRNAS996"
/lissue_type="egg, subtracted by stage 19-26 animal cap"
/lab host="mR108 (phage-realstant)"
/lone lib="Wellone CRC pRN3 Stl9 26 egg animal cap"
/note="Vector: pBSRN3; Site_1: Not!; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Welloome/CRC Institute). "
(Welloome/CRC Institute). "
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Best Local Similarity 100.0%; Pred. No. 4.4e-136;
Matches 290; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
/mol_type="mRNA"
/db="mRNA"
/db=xref="Laxon:8355"4
/tissue_type="egg, subtracted by stage 13-17 animal cap"
/tissue_type="egg, subtracted by stage 13-17 animal cap"
/lab host="mB10B (phage-resistent)"
/clone lib="Welloome CRC pRN3 St13 17 egg animal cap"
/note="Vector: pBSRN3; Site_1: Not1; Site_2: EcoRI; cDNAs
/were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Gazrett, E Bellefroid, and A.M.
Zorn, (Wellcome/CRC Institute). "
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Enteryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
I (bases I to 391)
I (bases I project, 1999
I (bases I base)
I (bases I 
                               Library constructed by N. Garrett, E. ellefroid, and A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stopp: 350.
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llarity 100.0%; Pred. No. 4.3e-136;
Conservative 0; Mismatches 0;
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          est@watson.wustl.edu
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93 c
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Expressed Sequence Tags from Reproductive Organs of Ipomoea trifida CDNA Libraries
Unpublished
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1 (bases 1 to 401)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Unpublished
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                               /organism="Ipomoea trifida"
/mol_type="mRNA"
/db_xref="!axon:3584"
/clone="ISM-0348"
/tissue_type="stigma"
/dev_erage="tri-nucleate pollen stage"
/clone lib="lpomoea trifida stigma"
a 107 c 109 g 102 t
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100.0%; Pred. No. 4.4e-136;
tive 0; Mismatches 0;
                                                                                        Contact: Tohru Tsuchiya
Faculty of Bioresources
Mie University
1515 Kamihama, Tsu, Mie 514-8507, Japan
Tel: 81-59-231-9515
Fax: 81-59-231-9515
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                                                                                                                                                                                                                       Email: tsuchiya@bio.mie-u.ac.jp.
Location/Qualifiers
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                                                      Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon, (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LiNL at: info@lmage.llnl.gov
High quality sequence stops: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="egg"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC pcDNAI egg"
/note="Vector: pcDNAI; Site_1: NOTI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Library was
constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute)."

102 c 105 g 89 t 2 others
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398 bp mRNA linear BST 21-OCT-2002
308 bp pp mRNA linear BST 21-OCT-2002
mRNA sequence.
AU224539.1 GI:24207512
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1 (Dases 1 to 398)
Tsuchiya, T., Ando, A., Ogawa, C., Futagami, K., Watase, T. and Kowyama
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3431758"
Waterston, R. and Wilson, R. WashU Xenopus EST project, 1999
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Best Local Similarity 100.0%
Matches 290; Conservative
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Ipomoea trifida
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/organism="Columba livia"
//organism="Columba livia"
//mol type="mRNA"
//mol type="mRNA"
//db_xref="taxon:8932"
//tissue_type="optic tecta"
//tissue_type="optic tecta"
//tissue_type="optic tecta"
//dev stages="10 day postnatal"
//clone lib="Differentially expressed cDNA library of optic tectum of pigeon with removal of left retina"
//clone="Differentially expressed cDNA library of optic fectum of pigeon with removal of left retina"
//clone="Differentially expressed cDNA library of optic fectum of pigeon with removal of left retina"
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1 (bases it to 418)
1 (bases it to 418)
2 (bases it to 418)
1 (bases it to 418)
2 (bases it to 418)
  Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, R., Gibbons, M., Harrey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
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Library constructed by N. Garrett, K. Ryan and A.M. Zorn,
(Wellcome/CRC Institute). DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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llarity 100.0%; Pred. No. 4.5e-136;
Conservative 0; Mismatches 0;
Shanghai Tiedao University Medical School
Googhexin Kd.1238, Shanghai, 20070, China
Email: jinroxia@public.sta.net.cn.
Location/Qualifiers
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Xenopus laevis
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BI941233.1 GI:16255705
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                                   Enail: est@watson.wustl.edu
Library constructed by N Garrett, E. ellefroid, and A.M. Zorn
(Wellcome/CAC Institute). DNA Sequencing by: Washington University
Genome Sequencing Center.

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
High quality sequence stop: 291.
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                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="egg, subtracted by stage 19-26 animal cap"
/lab_host="DH10B (phage-resistant""
/clone_lib="Wellcome CRC PRN3 S119 26 egg animal cap"
/note="Vector: pbSRN3; Site 1: Not!; Site 2: EcoR1; cDNAs
were oligo-dT primed and directionally cloned. Staging
were oligo-dT primed and firectionally cloned. Staging
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute). "
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Lu, L., Xu, L., Yang, C., Li, X. and Wang, Y.
A profile of differentially expressed genes in P10 pigeon optic tecta with removal of left retina after posthatching first day by
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                                                                                                                                                                                                                                                                                  /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4785984"
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Columba livia
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Department of Biochemistry
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Vigna unguiculata
Vigna unguiculata
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
surosids I, Pabales; Rabaceae; Papilionoideae; Phaseoleae; Vigna.
1 (bases 1 to 420)
Denny, R., Danesh, D., Mudge, J., Cooper, A., Larson, K., Fatokun, C. and RFLP sequences of cowpea, Vigna unguiculata
                                                 available
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Department of Plant Pathology
University of Minnesota
458 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
Tel: 612 625 2225
Fax: 612 625 9728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center Context Clones from this library are avail Clone distribution: Kenopus clones from this library are avail through the I.M.A.G.E. Consortium/LLNL at: infooimage.llnl.gov Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 336.

High quality sequence stop: 336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.0%; Score 290; DB 12; I
Best Local Similarity 100.0%; Pred. No. 4.5e-136;
Matches 290; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            organism="Xenopus laevis"
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AZ254218.1 GI:8602455
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SOURCE
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AZ254218
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Sequence of mapped RFLP marker cg0029 on linkage group vi of cowpea. For more information, see Beandenes at: http://ars-genome.cornell.edu/cgl-bin/MebAcc/webace?db=beangenes.cl ass=Locus. Please see as authorities for mapping/naming: Fatokun, C.A., Danesh, D., Young, N.D. (1993) RFLP linkage map for cowpea (vigna unguiculata (L.) Walp.) in: Genetic Naps., 1992. S. J. O'Brien, ed. Cold Spring Harbor Press, Cold Spring Harbor, NY, pp. 6.256.6.258 - and - Menancio-Hautea, D., Kumar, L., Danesh, D., Young, ND. (1993) RFLP linkage map for mungbean (vigna radiata (L.) Wilczek) in: Genetic Maps, 1992. S. J. O'Brien, ed. Cold Spring Harbor, NY, pp. 6.259-6.260.
Insert Length: 400 Std Error: 0.00
Seq primer: M13F
Class: RFLP probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / organism="Vigna unguiculata"

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/clone_lib="RFLP sequences of cowpea, Vigna unguiculata"
/note="Vector: pUC 18; Site 1: Pst I; DNA was digested
with Pst I, size separated by sucrose gradient
centrifugation and the fraction between S00-3000 base
pairs ligated into the vector using standard method. "
98 a 104 c 112 g 90 t 16 others
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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29.0%; Score 290; DB 28; L
Best Local Similarity 100.0%; Pred. No. 4.5e-136;
Matches 290; Conservative 0; Mismatches 0;
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BI937686
LOCUS
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Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, S., Gibbons, M., Harvey, N., Ritter, B., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.B. Consortium/LINL at: info@image.llnl.gov Bossible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco
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de33f05.x1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone IMAGE:3473792 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN. ;,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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100.0%; Pred. No. 4.5e-136;
iive 0; Mismatches 0;
                                                                                                                                                                                                     Unpublished
Contact: Sandy Clifton, Ph.D.
WashU Kenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. L
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Xenopus laevis
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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| / organism=records |
                                                                                                                                                                                                                                                                                                                                                                                          Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.B. Consortium/LIML at: info@image.llnl.gov Possible reversed clone: similarity on wrong strand sequencing: -40UF from Gibco.
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Xenopus laevis
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                  USA
                                                                                                  Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 17el: 314 286 1800
Fax: 314 286 1810
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ive 0; Mismatches 0;
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Location/Qualifiers
        Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wistl.edu
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Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@lmage.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from disco
High quality sequence stop: 379.
     Xenopodinae; Xenopus.
1 (bases 1 to 424)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Amatin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.; Person, Waterston,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
WashU Xenopus EST project, 1999
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/tissue_type="dorsal lip"
/tissue_type="dorsal lip"
/lab_nost="PHIOB (phage-resistant)"
/clone_lih="PHIOB (phage-resistant)"
/note="vector: pBSRN3; Site_1: Not1; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging were oligo-dT primed and directionally cloned. Staging by A.M. Zorn (Wellcome/CRC Institute). "
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                             Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4.5e-136;
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/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
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Email: est@watson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 309.
Location/Qualifiers
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                                                                                                                                                             Xenopodinae; Xenopus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fax: 314 286 1810
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Pred. No. 4.5e-136;
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100.0%; Prec
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/clone="IMAGE:3474380"
/tissue type="dorsal lip"
/tissue type="dorsal lip"
/tab_host="DH10B (bage-resistant)"
/clone lib="Wallcome CRC pRN3 dorsal lip"
/clone lib="Wallcome CRC pRN3 dorsal lip"
/note="Vector: pBsRN3; Site_1: Not1; Site_2: EcoR1; cDNAs were oligo-dT primed and directionally cloned. Staging ware oligo-t primed and directionally cloned. Staging by A.M. Zorn (Wallcome/CRC Institute). "
106 c 112 g 105 t lothers
                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
1 (Dases I to 424)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martin, J., Wylle, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Washu Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov Sesabble reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco
de41b11.x1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone IMAGE:3474380 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN: ;,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. L
442 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                    Xenopus laevis (African clawed frog)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Sandy Clifton, Ph.D.
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100.0%; Fit
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Best Local Similarity 100.
Matches 29.0, Conservative
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Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Wash, X., Mallons, EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Center
Sequencing by: Washington University Center
Clone distribution: Kenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@lmage.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 375.
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were cligo-dT primed and directionally cloned. Staging
were cligo-dT primed and Faber. Library was constructed
by A.M. Zorn (Wellcome/CRC Institute). "
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WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fas: 314 286 1810
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                                                                                 Xenopus laevis (African clawed frog)
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Length 424; Indels 128

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Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/Lub. at: info@image.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq prime: -40UP from Gibco
High quality sequence stop: 397.
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106 c 113 g 106 t
                                                BI938341 424 bp mRNA linear BST 18-OCT-2001 de41f04.x1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone IMAGE:3474558 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN. ;,
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
, Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
b., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
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29.0%; Score 290; DB 12; Length 424;
Best Local Similarity 100.0%; Pred. No. 4.5e-136;
Matches 290; Conservative 0; Mismatches 0; Indels (
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309 CCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTA 358
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Search completed: February 16, 2004, 03:15:45
Job time : 2640.53 secs

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February 15, 2004, 19:10:26; Search time 3961.99 Seconds (without alignments) 10335.846 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	V00618 Transposon I01012 Sequence 4	E02455 DNA encodin	AR067785 Sequence M84115 Cloning vec	U32991 Escherichia	AY048743 Template	A02231 Plasmid pDM	A02297 Plasmid pDM	A0/054 Artificial A10362 Artificial	A14595 Synthetic n	Alybua Arcificiai A30452 plasmid pDM	AR096518 Sequence	AR099244 Sequence	AR172638 Sequence AR207786 Sequence	AR218546 Sequence	AKZSJ199 Sequence AR266379 Sequence	AR267137 Sequence	BD093415 Antimicro	BD129548 Polynucle	BD134158 Vascular	BD134899 Apoptosis	AR134670 Sequence	AR219194 Sequence	Ax389681 Sequence AR134669 Sequence	AR219193 Sequence	AR266415 Sequence BD005772 Therapeut	AR207828 Sequence	AR134671 Sequence	A92666 Sequence 2	ARI37192 Sequence	AR130340 Sequence AR241208 Sequence			bp DNA linear BCT 02-562-1999 dding neomycin and kanamycin resistance	ily Liame or a ruthier b	resistance; transferase.	roteobacteria; Enterobacteriales;	.A., Reiss, B. and Schaller, H. ocalization of the neomycin
SUMMARIES	a	1 ISTN5X 6 I01012	E02455	AR067785 SYNKANRA	ECU32991	AY048743	A02231	A02297	AU/054 A10362	A14595	A19608 A30452	AR096518	AR099244	AR172638 AR207786	AR218546	AR253199 AR266379	AR267137	BD093415	BD129548	BD134158	BD134899	AR134670	AR219194	AX589681 AR134669	AR219193	AR266415 BD005772	AR207828	AR134671	A92666	AR137192	AR158346 AR241208	ALIGNMENT	;	1300 enco	or che	neomycin	seria; Gammaprot Escherichia.	nerswald, E
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                                          GCCAGGTAGCCGAATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGATACTT
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1 (bases 1 to 1300)
i Puhler.A., Rellaender,H. and Weber,G.
Nitrogen fixation regulator genes
L Patent: US 4782022-A 401-NOV-1988;
Lubrizol Genetics, Inc., Wickliffe, OH
Location/Qualifiers
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| ELQEWGGTWAALVDPDGT" |
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EHGGLAPAELFARLKAMPDGEDLVVTHGDACLPNIKVENGRFSGFIDGGRLGVADRY
QDIALATRDIAEELGGEWADRFLVVYGIAAPDSQRIAFYRLLDEFF"
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                                                                                             /organism="Escherichia |
/mol type="genomic DNA" |
/db xref="taxon:562" |
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904 GCGAATCGGGAGCGGCATACCGTAAAGCACGGGGAAGCGGTCAGCCCATTCGCCGCAA 241 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCA 844 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCA 301 GCCGGCCAACTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 784 GCCGGCCACAGTCGATGAATCCAGAAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 784 GCCGGCCACAGTCGATGAATCCAGAAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 361 AGGCATCGCCATGGGTCACGAAGAAACCTGCCGTCGGGCCATTGAGCCTGGG	24	GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCGCGTTGCATCAGCCATGACTATGGATACTTTGCATCAGCCATGACTATGGATACTTTGCATCAGCCATGACTATGCATCAGCCATCAGCGATACTTTTGCATCAGCCATCAGCCATCAGCATACATCATCATCATCATCAGATACTTTTCATCAGCAATAGCATACATA	661 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGACACACGCCGCAAGGAACGCCCGTCG 72 1	QY 721 TGGCCAGCCACGATAGCCGCGGTGCTCCTGCAGTTCATTCA	OY 781 CGGTCTTGACAAAAGAACCGGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG 840	OY 841 AGCAGCGATTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGGGCCG 900 Db 244 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCAAGCGGCCG 185	Qy 901 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTTTT 960 Db 184 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTGTTCTTTT 125	OY 961 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001	RESULT 3 E02455/c E02455/c LOCUS DEFINITION DNA encoding aminoglycoside 3'-phocphotransferaseII(APH). ACCESSION E02455	VEXACLON EVERS), GITAL/USES SCHWCES Transposen Th5 ORGANISM Transposen Th5 transposens.	AUTHORS YORHIDA, N., KIKUCHI, N., Shin, M. and Teraoka, H. TITLE MODIFIED HUMAN PSTI JOURNAL PATENT: JP 1990150282-A 1 08-JUN-1990;	COMMENT OS TRANSPOSON THE PN JP 1990150282-A/1 PD 08-JUN-1990

94 361 AGGCATCGCCATGGGTCACGACGACATCCTCGCCGTCGGCCTTGAGCCTGG 420 Db 1292 AGGCATCGCCATGGGTCACGACGACATCCTCGCCTTGGTTTTTTTT	QY 541 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCGCATTGCATCAGCCATGATGGATACTT 600 Db 1472 GGCAGGTAGCCGATCAGCGCGCGCGCATTGCATCAGCCATGATGGATACTT 1531 QY 601 TCTCGGCAGGAGCAAGGTAAACAGAGAAGATCCTGCCCCGGCACTTGCCCCAATAGCA 660 Db 1532 TCTCGGCAGGAGCAAGGTGAAGATGACAGGAGGATCCTGCCCCGGCAATAGCA 1591 QY 661 GCCGAGTCCCTTAGTGACAAGGTCAGGAGATCCTGCCCCGGCAATAGCA 1591 QY 661 GCCGAGTCCCTTAGTGAAAGGTCAAGGAGAACCTGGCCAAAGAACGCCCGTTG 720	Db 1592 GCAGTCCCTTCAGTGACAACGTCGAGACAGCTGGAGAACGCCGTCG 1651 721 TGGCCAGCCACCATCAGTGACAACGTCGACACAGTTCATTCA	SYNKANRA LOCUS SYNKANRA LOCUS LOCUS LOCUS Cloning vector pHSS6 kanamycin resistance protein (neo) gene, putative cds. ACCESSION M84115. ALITHE M44115. M44116. M44115. M44116. M44115. M44116. M4411
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Microbiology and Immunology, University of Adelaide, Frome Road,
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'function="kanamycin restistance gene from Th5"
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           'organism="unidentified cloning vector"
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                                                                                                                                                                                             Beck, E., Ludwig, G., Auerswald, E.A., Reiss, B. and Schaller, H. Mucleotide sequence and exact localization of the neomycin phosphorransferase gene from transposon Tn5 Gene 19 (3), 327-336 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transposon vectors containing non-antibiotic resistance markers for cloning and stable chromosomal insertion of genes in gram-negative bacteria

J. Bacteriol. 172 (11), 6557-6567 (1990)
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Pinyon, R.A. and Thomas, C.J.
DNA sequence of a mini-Tn5 transposon (mini-Tn5 Km)
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Datsenko, K.A. and Wanner, B.L. One-step inactivation of chromosomal genes in Escherichia coli K-12
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                            1190 retregecialgegialagargialagagagarectgececegeaerregeearagea 1131
                                                                                          TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCCAATAGCA 660
                                                                                                                                                                             GCCAGICCCTICCCGCTICAGIGACAACGICGAGCACAGCIGCGCAAGGAACGCCCGTCG 720
                                                                                                                                                                                                                                                                                                                                                      CGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGGGCGTCAG 840
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    541 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCATTGCATCAGCCATGATGGATACTT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       950 AGCAĞÖCĞATTGTCTGTTĞTĞCCCAĞTCATAĞCCĞAATAĞCCTCTCCACCCAAĞCĞĞCCĞ 891
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2 (Dases 1 to 3267)

Datesnko K.A. and Wanner, B.L.

Direct (Submission

Submitted (29-UUL-2001) Biological Sciences, Purdue University,

Lilly Hall of Life Sciences, West Lafayette, IN 47907, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                              using PČR products
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6640-6645 (2000)
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/transi_table=1!
/product="Tn5 neomycin_phosphotransferase"
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/db_xref="G1:15554333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       961 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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Template plasmid pKD4, complete sequence.
AY048743
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/note="kanamycin resistance"
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/note="natural FRT site"
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/db_xref="taxon:170492"
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Template plasmid pXD4
artificial sequences; vectors.
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/product="neomycin phosphotransferase"
/protain_id="AAABS506_11"
/db_xref="id:-1000123"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSSHLAPAEKVSIMADÅMRRLHTLDPATCPFDHQAKRRIERARTRNBAGLVDQDDLDE
EHQGLAPAELFARIKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY
QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
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, 1996 this sequence version replaced gi:1000122.
Location/Qualifiers
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/note="Tn5 O end functional in transposition"
/citation=[4]
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note="Tn5_I end functional in transposition"
                                                                                                                                                                                                                                                                                                                57. T.1651
function="neomycin and kanamycin resistance"
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                                                                                     /organism="Escherichia coli"
/mol_type="genomic DNA"
/strain="SMIO (lambda pir)"
/db_xref="taxon:562"
/plasmid="mini-Tn5 Km"
/transposon="mini-Tn5 Km"
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       Adelaide, S.A. 5001, Australia
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Best Local Similarity
                            On Jan 23,
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  912 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGATG 853
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                                             GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT
                                                                                  852 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT
                                                                                                                             601 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA
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Plasmid pDMI,1 DNA sequence from patent EP0309746.
A00782
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
1 1035 c 1056 g 836 t
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Patent: BP 0309746-A 11 05-APR-1989;
F. HOFFMANN-LA ROCHE AG
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ive 0; Mismatches
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EHGGLAPAELFARIKARWPDGEDLVYTHGDACLPNIKVENGRESGFIDGRLGVADRY
QDIALATRDIAEELGGEWADRFLVVLYGIAAPDSQRIAFYLLDEFF"
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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASROCLIDWMEADKVAGPL
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/translation="MSIQHFRVALIPPFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
/translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR
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/note=rrnB transcription terminator"
/note=rrnB 869 g 807 t
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complement(1979. .2839)
/note="bla; ampicillin resistance"
                                                                                                    529. .548
/note="common priming site kl"
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/note="common priming site kt"
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/note="FRT site"
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FRATURES 13740 Source // .3740 // Sequiam="synthetic construct" // mol_type="genomic DNA" // Mol_type="genomic DNA" // And type="genomic DNA"	Ouery Match 100.0%; Score 1001; DB 6; Length 3740; Best Local Similarity 100.0%; Pred. No. 0; Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps	1 CGCTGGAGGATCATCCAGCGGCGTCCCGGAAACGATTCCGAAGCCGACCTTTCATAG	61 AAGGCGCGCTGGAATCGAAATCTCGTGATGGCAAGTTGGCCGCTTGGTCGGTC	121 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT	181 GCGANTCGGGAGCGCCCATACCGTAAAGCACGAGGAAGCGCTCAGCCCATTCGCCGCCCAATCGCGGCGATACCGTAAAGCACGAGGAAAGCGCGCCATTCGCCGCCAATCGCGGCGATACCGTAAAGCACGAGGAAAGCGCGCTCACCCATTCGCCGCCAA	GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAA		Oy 361 AGGCATCGCCATGAGTCACGACAATCCTCGCCGTCGGGCATGCGCCCTTGAGCCTGG 420		QY 481 GACCGGCTTCCATCCGAGTACGTGCTCGATGCGATGTTTCGCTTGGTGGTCGATG 540		OY 601 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCA 660	QY 661 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGGACGCCCAAGGACGCCCGTCG 720 Db 630 GCCAGTCCCTTCCCGCTTCAGTGACATCGAGCAACGTGCGCAAGGAAACGCCCGTCG 571	Qy 721 TGGCCAGCCACGCGCTGCCTCCTCCTGCAGTTCATTCAGGGCACCGGACAGGT 780	OY 781 CGGTCTTGACAAAAGAACCGGGGCCCCTGCGCTGACGCGGAACACGGGGCTTCAG 840 [QY 841 AGCAGCGARTGTCTGTTGTGCCGAGTCATAGCCGAATAGCCTCTCCACCCAAGGGGCG 900
OY 181 GCGRATCGGGAGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA 240 Db 1110 GCGATTCGCGGTAACGTAAAGCACGAGAAGCGAAACGCCTTTGCCGCCAATTCGCCGCCAA 1051 QY 241 GCTCTTCACCAATATCACGGTAACCAAGCTATGTCCTGATAGCCGCACACCCA 300 Db 1050 GCTCTTCAGCAATATCACGAGTAACCAAGCTATGTCCTGATAGCCGCCACACCCA 300	GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC	QY 361 AGGCATGGCCATGGGTCACGAGATCCTCGCCGTCGGGCATGCGCGCTTGAGCCTGG 420 DD 930 AGGCATGGCCATGGGTCACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG 871	421 CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCGACAA 480	TCGAATG TCGAATG	541 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCATTGCATCAGCCATGATGATACTT 600	601 TCTCGGCAGGAAGGTQAGATQACAGGAGATCCTGCCCCGGCACTTGGCCCAATAGCA 660	000000 	GACAGGT - - - - GACAGGT	GCATCAG GCATCAG		901 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGGGAAGGATCCTCATCCTGTCTCTT	Oy 961 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGC 1001	7)990,090,1131,000,1100,000,1100,1131,000,1100	ACCESSION A02231 DEFINITION Plasmid pDMI,1 DNA. 3740 bp DNA linear PAT 30-APR-1996 DEFINITION A02231 VERSTON A02231 A02231 GT:490290		Arthora arthroxal Sequences. AUTHORS Doebeli,H., Eggimann,B., Gentz,R., Hochuli,E. and Stueber,D. AUTHORS Preion proteins and their purification JUTLE Freion; EP 0282042-A 5 14-SEP-1988; F. HOFFMANN-LA ROCHE AG

Tue Feb 17 08:46:04 2004

0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		QY 661 GCCAGTCCCTTCCGGCTTCAGTGACACGCTGAGCACACGCGGCAGGAACGCCCGTCG	Db 510 CGGTCTTGACAAAAAGAACCGGGGCGCCTGGCGTGACAGCGGGGGGCGCGGGGGGGG	QY 901 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGGGAAACGATCCTGTTCTT 960 GAGAACCTGCTGTGTTCATCATGTTGAATCATGTTGATGTTGATGTTGATGTTGTTGATGTTGTTGTTGT	DB 6; Length 3740; A07054/c O; Indels O; Gaps O; DEFINITION Artificial sequence neo and lact gene for neomycin par 25-AUG-1993 ACAUTTCGAAGCCGAAGCTTTCATAG 60		ATGCGCT 180 ATGCGCT 180 AUTHORS DOE TITLE HOM ATGCGCT 1111 DAE DOE TOURNAL PAR	CCGCCAA 240 CCGCCAA 1051 SOURCE ACACCCA 300		Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 420 Oy 1 CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCTTTCATAG	TCGACAA 480 DB 12590 Qy 61 CGACAA 811 Db 1230	1230
Db 30 A A A A A A A A A A A A A A A A A A		3740 bp DNA GI:345260		av _	100.0%; Score 1001; 100.0%; Pred. No. 0; vative 0; Mismatches						421 CGAACAGTTCGGCTGGGGGGGGAGCCCTGATGCTCTTGGTCCAGATCATCCTGA 	481 GACCGGCTTCCATCCCAGTACGTGCTCGCTCGATGCTTTTCGCTTGGTGGTCGAATG

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                     GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCCCCACCCCA
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Bujard, H. and Lanzer, M.
High repressible sequence for control of expetent: EP 0303225-A 9 22-FEB-1989;
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/organism="synthetic construct"
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/db_xref="taxon:03630"
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banwarth, W., Caspers, P., Le Grice, S. and M Recombinant HIV-2 polypeptides
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F. HOFFMANN-LA ROCHE A6 24-MAY-1989;
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Bannwarth, W., Certa, U., Mous, J. and Stueber, D.
Polypeptides that elicit antibodies against AIDS virus
Patent: EP 0219106-A 8 22-APR-1987,
F. HOFFMANN-LA ROCHE AG

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1 (bases 1 to 3740)
Fountoulakis, M., Garotta, G. and Stueber, D.
Soluble interferon-gamma receptors and methods for their production
Patent: EP 0393502-A 16 24-0CT-1990;
F. HOFFMANN-LA ROCHE AG
Location/Qualifiers
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DT 25-MAR-2003 (updated)
DT 15-SEP-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of novel vector plasmid pUNI-10. It includes: the conditional origin of replication from R6K-gamma, derived from plasmid R6K (ATCC 3720); a Not1-Kpn1 polylinker that derilitates the exchange of Lox sites; a wild-type loxP site (see also AAZ58066); a polylinker used for the insertion of genomic DNA or CDNA sequences; a bovine growth hormone polyA site; a T7 terminator; and a kanamycin removed the native Nool site. pUNI-10 is an example of novel Univertors or pUNI vectors of the invention that have a sequence-specific recombinase target site (e.g. loxP) preceding the insertion site for the gene of interest, a selectable marker gene (optional) and a conditional origin of replication that is active only in host cells expressing the requisite transacting replication factor (optional). The vectors are designed to contain a gene of interest but to lack a prometer for expression of the subcloning of nucleic acid sequences. The method is referred to subcloning of nucleic acid sequences. The method is referred to subcloning of nucleic acid sequences. The method is referred to subcloning of nucleic acid sequences. The method is referred to subcloning of nucleic acid sequences. The method is referred to subcloning of nucleic and sequences. The method is referred to subcloning of nucleic and sequences. Publication events are genetically selected and result in placement of the gene of interest under the control of novel regulatory elements. A second Ups-related method allows for the precise transfer of coding sequences alone from subcloning of entire nucleic acid libraries and the directional cloning of linear nucleic acid libraries and the directional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New methods for recombination of nucleic acid constructs, useful for the rapid subcloning of nucleic acid sequences in vivo and in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1001; DB 21; Length 2220; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                               /*tag= g
/note= "kanamycin resistance gene from Tn5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2220 BP; 506 A; 610 C; 581 G; 523 T; 0 other;
                                  /*tag= e
/note= "BGH polyA site"
                                                                                                                                                                                  terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 44; Page 63-64; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US15481.
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/note= "T7 t
896..2220
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Best Local Similarity 100.
Matches 1001; Conservative
                                                                                                      51..890
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                                                                                                                                                                                                                prim_transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1998;
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polyA_site
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1100 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCA 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence shown is that of a novel transposon useful for sequencing long DNA sequences. The transposon comprises a partial sequencing long DNA sequences. The transposon comprises from phages SP6 and T7 inserted near the opposite ends of Tn5. At each terminus a segment of 19 nucleotides of either the O-end or I-end of Tn5 are present and restriction enzyme sites are positioned throughout the sequence (esp. with one at either end, less than 20 bases from each terminal segments of Segments of foreign DNA of at least 17 bases are positioned directly adjacent to each restriction site. The transposon also comprises a Tn5 transposase gene insert and a kanamycin selectable marker for the transposable DNA unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1340 CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAACGATTCCGAAGCCCAACCTTTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1280 AAGGCGGCGGCGAAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGAATCGGGAGGCGCGATACCGTAAAGCACGAGGAAAGCGGTCAGCCCATTCGCCGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1160 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 1001; DB 14; Length 3176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bidirectional sequencing of long DNA molecules - by inserting transposon Tn5seq1 into DNA molecule of E coli cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3176 BP; 661 A; 898 C; 893 G; 724 T; 0 other;
                                                                                                                                          /*tag= z
/note= "O-end of Tn5 transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGT
                                                                               /*tag≈ y
/note= "BamHI site"
3158..3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 4; 17pp; English.
                     '*tag= x
'note= "SP6 :RNA"
1142..3147
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90US-0508379,
3042..3157
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                                                          misc_feature
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12-APR-1990;
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misc_RNA
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note= "codes for kanamycin selectable marker"
                                                                                                                transposon sequence
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note≃ "tnp (Tn5 transposase gene)"
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note= "Eco47III restriction site"
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/*tag= f
/*tag= f
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/*tag= g
//note= "SphI restriction site"
/*tag= h
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/*note= "NCOI restriction site"
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note= "HindIII restriction site"
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T-tag= c
Tote= "BamHI restriction site"
76.381
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tag= j
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note= "SacII restriction site"
856..2861
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10te= "AvaII restriction site
                                                                                                                                                                                                                                                                           *tag= d
note= "Bcll restriction site"
07..1201
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note= "NruI restriction site"
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note= "SalI restriction site"
omplement (1549..2979)
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note= "XhoI restriction site"
611..2617
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note= "SapI restriction site"
881..2886
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note= "Hpal restriction site"
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note= "NheI restriction site"
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note= "NotI restriction site'
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lote= "BsmI restriction site'
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note= "SmaI restiction site"
                                                 ocation/Qualifiers
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/note= "O-end Tn5
complement (1..29)
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1220 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGAGGCGATAGAAGGCGATGCGCT 1161
                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the ThSseq1 transposon used in the method of the invention. The method is for RNA transcription, and comprises the insertion of the ThSseq1 transposon into an E. coli DNA molecule to obtain hyperexpression of genes adjacent to strong promoters SP6 or T7. The transposon is useful for stimulating the transcription of genes adjacent to the heterologous SP6 or T7 promoters in E. coli, for making RNA transcripts in vitro and the hyperexpression or specific transcription of genes (adjacent to the SP6 or T7 ends) in vivo. ThSseq1 offers a less laborious method of sequencing long DNA molecules than current methods such as base-specific chemical cleavage and enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1340 CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 CGAACAGTTCGGCTTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 GCTCTTCAGCAATATCACGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCA
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                                                                                                                                                                                                                                                                 Obtaining hyperexpression of genes in Escherichia coli hosts insertion of transposon Tn5seq1 such that the strong SP6 and promoters are adjacent to the host genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3176 BP; 661 A; 898 C; 893 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGCCCACAGTCGATCCAGAAAAGCGGCCATT
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                                                                           87US-0105422.
90US-0508382.
93US-0004406.
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                                                                                                                                                                                                                               WPI; 1999-152772/13
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                                                                           05-OCT-1987;
12-APR-1990;
14-JAN-1993;
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                                         14-JAN-1993;
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/note= "specifically claimed region (claim 1)"
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strong promoter; SP6 promoter; T7 promoter; ss.
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                                                                                                                                                                                                                                                                                                             Transposon Insseq1 was constructed from the pBR322-derived plasmid pBR322:3C1:ThE. The novel transposon is contained in plasmid pBRG1408. Ican be used for sequencing bacterial genomic DNA without recombinant DNA cloning and also for sequencing DNA cloned in phages or multicopy plasmids. It may also be useful for RNA sequencing with SPG and IT RNA polymerases, for making RNA transcripts in vitro and for hyperexpression or specific transcription of adjacent genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 3177;
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screening of DNA sequences
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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                Claim 3; Fig 4; 19pp; English
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        GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATAGTTA
                                                                      TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA
                                                                                             TCTCGGCAGGAGGAAGGTGAGATGACAGGAGATCCTGCCCCGGGCACTTCGCCCAATAGGA
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Phage T7; RNA polymerase; DNA sequencing; ss.
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                                        Plasmid encodes a fusion protein consisting of 1 or 2 affinity peptides bonded directly or consisting of 1 or 2 affinity peptides bonded directly or indirectly to a biologically active protein (i.e. dihydrofolate reductase). The presence of adjacent His residues in the affinity peptides allows purificn of the biologically active protein by metal-chelate chromatography on nitrilocritacetic acid resins. See also AAP80401-3 and AAN80955-8 and AAN80960-63. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                       9; Length 3740;
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                                                     GAGAACCTGCGTGCAATCCATCTTGAATCATGCGAAACGATCCTCATCCTGTCTTT
                                                                   390 GAGAACCTGCGTGCAATCCATCTTGAATCAATGGAAACGATCCTGTGTCTTT
                       CGCTGGAGGATCATCCAGCCGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAG
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                                                                                                      GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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*tag= a
/note="DNA encoding neomycinphosphot/1532..2611
/*tag= b
/note="DNA encoding lac repressor."
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cive 0; Mismatches 0;
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AAN81154 standard; DNA; 3740
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Best Local Similarity 100.
Matches 1001; Conservative
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09-JAN-2003
12-NOV-1990
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                                                                                GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCC
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                                                  HTLV-III; env protein; gag protein; AIDS; immunogenic activity;
vaccines; diagnosis; oligonucleotides; pDMI.1; neo-gene; lacl-gene; ss.
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E.Coli transfected with pDS5/RBSII,33+5A (AAN80481), pDS8/RBSII (AAN80482) or derivatives, cantg. a HTLV-gene, also contain plasmid pDMII. Expression is possible by addition of IPTG to the medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide with immunogenic activity of HTLV 3 env-gag protein - useful in vaccines and for AIDS diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lacl-gene: P.J. Farabaugh, Nature 274, 765-769 (1978) contg. the mutation Iq (M.P. Calos, Nature 274, pp. 762-765 (1978) for the lac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene is added.

The DNA encodes peptides useful as active ingredients in vaccines and for detecting AIDS antibodies in serum etc.

See also AAN80480-85.

(Updated on 25-WAR-2003 to correct PD field.)

(Updated on 25-WAR-2003 to correct PR field.)

(Updated on 25-WAR-2003 to correct PR field.)

(Updated on 25-WAR-2003 to correct PR field.)
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.larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0;
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kanamycin resistance of E.coli.
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               the neo-gene of Ins and the lacl-gene.
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product=neomycinphosphotransferase
1532.2611
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                                                                                                                                                                                                                                                                                                                                                                                                                                               )5-DEC-1986;
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Best Local Simi
Matches 1001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repressor.
                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                GAGAACCTGCGTGCAATCCATCTTGTTCATGCGAAACGATCCTCATCCTGTCTTT 960
                                                                                                                                                                                                                                                                                                                                      331
    GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGAATG
                                                     GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG
                                                                                                                                              GCCAGTCCCTTCCGCTTCAGTGACAACGTCGAGCACAGGTGGCGCAAGGAACGCCCGTCG
                                      GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGCATACTT
                                                                                  TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGGCACTTCGCCCAATAGCA
                                                                                                                                                                                       781 CGGTCTTGACAAAAAAAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
                                                                                                                                                                                                                                                                   AGCAGCCGATTGTCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                                          AGCAGCCGATTGTCTGTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                                                                                                                                                                                             390 GAGAACCTGCGTGCAATCCATCTTGTTCAATCAAGGAAACGATCCTCATCCTGTCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 1.2 kb insert from lambda 5-7 was isolated, ends were repaired with Klenow polymerase and BamHI linkers were ligated to both ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding it .
                                                                                                                                                                                                                                                                                                                                                          961 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                                                                                                                                                                                                                                                                                       330 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merozoite; antigen; vaccine; coccidiosis; RBS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen (23kD), D
in the prodn. of
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AAQ12786 standard; DNA; 3740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
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recombinant virus, useful
coccidiosis in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-224487/31
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09-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1170 TCGAACCCCAGAGTCCCGCTCAGAACTACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                       IFN-gamma is a therapeutically active agent in the treatment of autoimmune disease, allograft transplant rejections, multiple sclerosis, chronic inflammations and delayed hypersensitivity. It also useful in identifying IFN-gamma agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1001; DB 11; Length 3740;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                      treating auto-immune
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3740 BP; 813 A; 1035 C; 1056 G; 836 T; 0 other;
                      /*tag= a
/label= Neomycin phosphotransferase.
complement(1531..2609)
                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                 Soluble interferon-gamma receptors - for diseases, chronic inflammations, etc.
                                                       /*tag= b
/label= lac repressor.
                                                                                                                                                                                                         Ä
                                                                                                                                                                                                        Stuber
 Location/Qualifiers
357..1146
                                                                                                                                                                                                                                                                                    Disclosure, Fig 16; 174pp, English.
                                                                                                                                                                              (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                       Garotta G,
                                                                                                                                                          90EP-0106992.
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                                                                                                                                                                                                                            WPI; 1990-322042/43.
                                                                                                                                                                                                     Fountoulakis M,
                                                                                                                                                         11-APR-1990;
                                                                                                            24-OCT-1990
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This sequence represents the plasmid pDMI.1. This plasmid was used in conjunction with the expression plasmids pDS56/RBSII, -1, and -2. These plasmids contain the regulatable promoter/Operator element (N250FSMISOFS) and the ribosomal binding sites (RBS) RBSII, RBSII(-1) and RBSII(-2) respectively. These RBS are derived from the RBS of the promoter pg25 of the B. coli phage TS. These plasmids may be maintained in E. coli play if the promoter/operator element is repressed by the binding of a lac repressor to the operator. The lac repressor is encoded by the laci gene. NZ50FSMISOFSOR can be repressed efficiently only when a sufficient amount of repressor molecules are present in the cells. Therefore the lacid allele, which contains a promoter mutant responsible for increased expression of the repressor contains the neowych phosphotransfearse gene from the plasmid pACYC184 which contains all the information required for the plasmid between bases 1-1120 contains the replication and stable transmission to daughter cells. The region of these plasmids between bases 1-1120 contains the replication region and the gene for beta-lactamases gene is mediated by elimination of the HinoIII and PetI cleavage sites. These plasmids between plasmids all the enzymes Sall, PetI and HinoIII, also contain cleavage sites the enzymes Sall, PetI and HinoIII,
                                                                                   GAGAACCTGCGTGCAATCCATCTTGATCATGCGAAACGATCCTCATCTGTCTTT
                              450 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                              390 GAGAACCTGCGTGCAATCCATCTTGATCATGCGAAACGATCCTCATCCTGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid; pDS56/RBSII; -1; -2; regulatable; promoter; operator; N250PSN250P29; ribosomal binding site; RB5; RBSII; RBSII(-1); RBSII(-1); PQ25; E. coli; phage; T5; lac; repressor; lacI; lacIq; pDMI.1; replication; beta-lactamase; terminator; lambda; CAT; T1; chloramphenicol acevyltraneferase; rrnB operon; reading frame; neomycin phosphotransferase; Tn5; transposon; selection marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic specified polypeptide and fragments - capable inducing an immune response against eimeria parasites and from proteins produced by these parasites
                                                                                                                                                                                                      1001
                                                                                                                                                                                                                                                             290
                                                                                                                                                                                                                                        GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
                                                                                                                                                                                                      GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
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13-MAY-1993
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The modified fragment was inserted into each of pDS56/RBSII, pDS56/RBSII-1, and pDS56/RBSII-2. Plasmids contg. the inserts in both possible orientations were transformed into E. colistrain MIS carrying the compatible pDMI.1. The E. colistrain MIS contg. plasmids pSD56/RBSII and pDMI.1 is described in EP-316695.
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                                                                                                                                                                                                                                                                                                                                                 Length 3740;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                   Sequence 3740 BP; 809 A; 1039 C; 1056 G; 836 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                        (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1001;
100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 1001; Conservative
                                                                                                                                                                                                   See also AAQ12782-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thymus receptor tyrosine kinase; TRIK; LERK; Eph; colon carcinoma; testicular carcinoma; pancreatic carcinoma; lung adenocarcinoma; breast carcinoma; heptacellular carcinoma; cancer; cell proliferation; diagnosis; therapy; prognosis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated thymus receptor tyrosine kinase - is used to develop products for the diagnosis and treatment of cancers and other diseases involving aberrant cell proliferation
                                                                                                         GAICAGAICITGAICCCCTGCGCCAICAGAICCTTGGCGGC 1001
                                                                                                                                       GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 290
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                                                                                                                                                                                                                                                               Gaps
                               of the
the terminator of E. coli phage lambda, the promoter-free gene of chloramphenical acetyltransferase (CAT) and the terminator T1 of the E. coli trnB operon. These plasmids differ by one nuclectide following the ATG start color resulting in protein expressio in all three potential reading frames. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                               Sequence 3740 BP; 813 A; 1035 C; 1056 G; 836 T; 0 other;
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                                       3479 GAGAACCTGCGTGCAATCCATCTTGAATCATGCGAAACGATCCTCATCCTGTCTCTT 3538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of plasmid pHB4a (ATCC 209645). It includes a neomycin phosphotransferase gene as selectable marker, an Bscherichia coli origin of replication, a TS phage promoter sequence, 2 lac operator sequences, a Shine-Delgarno sequence, the lactose operon repressor gene (lacig) and a multiple cloning set lite linker region. A nucleotide sequence (see AAV66356) coding for novel human cardiac and pancreatic protein (ARP, see AAW80212) can be operatively linked to the promoter and operator (see AAV66373) of pHB4a, and CAPP expressed in E. coli cells following IPTG induction. CAPP polypetides can modulate the differentiation and products can be used in the diagnosis and treatment of pancreatitis and conditions that cause abnormal hypertrophy of the heart, such as hypertension, mycoardial infarction, valve disease and cardiomyopathy. The products can also be used in detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2579 CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAAACCTTTCATAG
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                                                                                                                                                                                                                                                                                                                                                                     Cardiac and pancreatic protein; CAPP; muscle-derived growth factor; human; pandreatitis; myocardial infarction; cardiomyopathy; vector; pHE4a; ds.
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100.0%; Pred. No. 0;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated cardiac and pancreatic protein
products for the diagnosis and treatment of
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Chimeric - bacteriophage T5.
Chimeric - synthetic.
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                                                                                                                                                                                                                Gaps
polypeptides in bacterial host cells
                The invention provides TRTK polynucleotides and polypeptides, vectors, host cells and recombinant methods of producing these. Also provided are diagnostic methods for detecting disease states associated with the aberrant expression of TRTK and therapeutic methods for treating such disease states, especially cancer.
                                                                                                                                                                       100.0%; Score 1001; DB 19; Length 3974; 100.0%; Pred. No. 0;
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production of recombinant TRTK
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Matches 1001; Conservative
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ELL2 RNA polymerase II elongation factor - and antibodies; for the prevention and treatment of neoplastic disorders, e.g. leukaemia
                                                      polymerase II elongation factor; human; neoplastic inhibitor; diagnosis; susceptibility; ds.
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                                                                                                                                                                                                                                                                                                    HUMAN GENOME SCI INC.
OKLAHOMA MEDICAL RES FOUND.
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This sequence is plasmid pHE4-5 which is used in a method to isolate and characterise a human RNA polymerase II elongation factor ELL2 which can be used in the design of treatments for neoplastic disorders (especially leukaemias). Antagonists of the polypeptides or nucleic acids that inhibit the expression of the protein, can be used to inhibit ELL2 susceptibility to neoplastic disorders comprises assaying ELL2 association level in mammalian cells or body fluid and comparing these expression level in mammalian cells or body fluid and comparing these indicates an increased or decrease or decrease in levels indicates an increased or decreased susceptibility. The gene expression level is assayed using the antibody, or by detecting ELL2 mRNA levels. The host cells of may be used to identify compounds which bind to an
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The present sequence represents pHE405 vector which contains human myelin oligodendrocyte glycoprotein-like protein (MOGp). The presence of MOGp on the surface of oligodendrocytes is associated with oligodendrocyte maturation and with the production of myelin. Products from the present invention can be used for the diagnosis, prognosis and treatment of e.g. cancers, inflammation, or demyelinating disease such as multiple sclerosis.
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lac operators, a Shine-Dalgarno sequence, and the lactose operon repressor gene (lacid). The newly isolated human breast cancer specific gene 1 (BGSP1). The newly isolated human breast cancer the promoter and operator by insertion between the Ndel and Asp718 aftes of the vector, allowing recombinant production of BGSP1 polypeptide (see AAM61213) in host calls. BGSP1 is useful as a breast cancer progressive marker. BGSP1 polymucleotides, bolypeptides and antibodies can be used to develop products for the diagnosis, clinical management and treatment of breast cancer and metastasis.
                                                                                                        Sequence 3974 BP; 899 A; 1116 C; 1095 G; 864 T; 0 other;
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                   CGGTCTTGACAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
                                                                                            GAGAACCIGCGAGCAATCCATCTTCAATCATGCGAAACGATCCTCATCCTCTT
                                                                                                               GAGAACCTGCGTGCAATCCATCTTGTTCATGCGAAACGATCCTCATCCTGTCTTTT
                                                                                                                                                                                                                                                                               human; metastasis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human breast cancer specific gene - used to develop products for the diagnosis, clinical management and treatment of breast cancer and marksrases
                                                                                                                                            GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
                                                                                                                                                                                                                                                                              Breast cancer specific gene 1; BCGS1; hur
therapy; genetic marker; vector; pHE3-4;
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100.0%; Score 1001; DB 19; 100.0%; Pred. No. 0;
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Sequence 1, Application US/08664224

Batent No. 5851808

GENERAL INFORMATION:
APPLICANT: Elledge, Srephen J.
APPLICANT: Liu, Qinghua
TITLE OF INVENTION: Recombination
NUMBER OF SEQUENCES: 18
CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Median & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: United States of America
STATE: LBM FCO Montgomery Street, Suite 2200
COUNTRY: United States of America
STATE: LBM FCO Montgomery Street, Suite 2200
COUNTRY: United States of America
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSSIFICATION NUMBER: US/08/864,224
FILING DATE:
RESIFICATION NUMBER: GOOFTWARE: A0,027
REFERENCE/DOCKET NUMBER: BCM-02681
TELECOMMUNICATION INFORMATION:
TELEFONDE (415) 397-8338
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US-09-30-1925-3

US-09-30-1925-3

US-09-30-193-27

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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 397-3338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2220 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 14, Appli
Sequence 13, Appli
Sequence 50, Appli
Sequence 50, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 9, Appli
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Patent No. 5212080
Sequence 33, Appl
Sequence 16, Appli
Sequence 7, Appli
                                                                                   February 15, 2004, 10:22:55; Search time 73.6147 Seconds (without alignments) 6001.851 Million cell updates/sec
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Sequence 21, P
Sequence 21, P
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2: /cgn2_6/ptodate/2/lna/5B_COMB.seq:*

3: /cgn2_6/ptodate/2/lna/6B_COMB.seq:*

4: /cgn2_6/ptodate/2/lna/6B_COMB.seq:*

5: /cgn2_6/ptodate/2/lna/PCTUS_COMB.seq:*

6: /cgn2_6/ptodate/2/lna/PcTUS_COMB.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-042-105-16

US-09-042-856A-7

US-09-044-856A-7

US-09-024-856A-7

US-09-026-408-14

US-09-026-408-14

US-09-027-154-4

US-09-027-154-9

US-09-03-106A-10

US-09-03-106A-11

US-09-03-11-11

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US-09-125-460A-11

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Gapop_60.0 , Gapext 60.0
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Match Length
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AGAAAAGCGGCGATTTTCCACCATGATATTCGGCAAGC 360 CCCTGATGCTCTTCGTCCAGATCATCTGATCGACAA 480 AGATOCTOGCOGTOGGCCATGCGCCCTTGAGCCTGG 420 540 SAGATICTCGCCGTCGGCCATGCGCCCTTGAGCCTGG 921 600 GCTCGCTCGATGCTTTCGCTTGGTGGTCGAATG 801 741 GACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA 660 780 840 GACAGGAGATCCTGCCCCGGCACTTCGCCCCAATAGCA 681 720 561 501 TGCAGCCGCCATTGCATCAGCCATGATGGATACTT TECAGCCGCCGCATTGCATCAGCCATGATGGATACTT GCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG ACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG GCCTCGTGCAGTTCATTCAGGCCACCGGACAGGT GCCTCGTCCTGCAGTTCATTCAGGCACCGGACAGGT 8686

5212080-1/c
;Patent No. 5212080
; APPLICANT: NAG, DILIP K., HUANG, HENRY V.;BERG, DOUGLAS E.; TITLE OF INVENTION: METHOD OF DNA SEQUENCOM=NG USING DNA; TRANSPOSON INSSEQL
; NUMBER OF SEQUENCES: 6

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2879 GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 2938
                                                                                                        2939 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCCTTGAGCCTGG 2998
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181 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
                                2759 GCGAATCGGGGGCGGCGGTAACCGTAAAGCACGAGGAGGGGGTCAGCCCATTCGCCGCAA
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US-09-042-105-16

Sequence 16, Application US/09042105

Sequence 16, Application US/09042105

Patent No. 6040157

GENERAL INFORMATION:

APPLICANT: HU, JING-SHAN

APPLICANT: ROSEN, CRAIG A.

APPLICANT: ROSEN, CRAIG A.

APPLICANT: CAO, LIANG

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROW
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 NEW YORK AVENUE

CITY: WASHINGTON

STATE: DC

COUNTRY: USA
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          GAGAACCIGCGIGCAAICCAICTIGITCAAICAAGGAAACGAICCICAICCIGI
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                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: DUAN, D. ROXANNE
APPLICANT: SHILATIFARD, ALI
APPLICANT: CONAMAY, JOAN W.
APPLICANT: CONAMAY, RONALD C.
TITLE OF INVENTION: RLL2, A New Member of an ELL Family of INVENTION: RLL2, A New Member of an ELL Family of ITLLE OF INVENTION: RAP Polymerase II Blongation Factors NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                        STREET: 1100 NBW 10CA AVENCE, CLIT: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-334
ZIP: 20005-334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,343
FILING DATE: Herewith
CLASSIFICATION OF PEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REPERRORS/DOCKET NUMBER: 1488.0880001
TELEPHONE: (202) 372-2540
INPORMATION POR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TTELEMEN: 1374 base pairs
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
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US-09-026-343-33
Sequence 33, Application US/09026343
Patent No. 6008018
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STRANDEDNESS: both
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MOLECULE TYPE: CDNA
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3059 GACCGGCTTCCATCCGAGTACGTCGCTCGATGCCATGTTTCGCTTGGTGGTCGAATG 3118
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Patent No. 6075124
GENERAL INFORMATION:
APPLICANT: LI, HADDONG
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP.
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                 481 GACCGCCTTCCATCCGAGTACGTCGCTCGATGCGATGTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,856A
FLING DATE: HEREWITH
CLASSIPICATION DATA:
APPLICATION NUMBER: US 08/726,830
FRICK APPLICATION DATA:
APPLICATION NUMBER: 08/479,126
FILING DATE: 07-04N-1995
FILING DATE: 21-APR-1995
FILING DATE: 21-APR-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: PSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTONNEY, AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 16;
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
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3479 GAGAACCIGCGIGCAAICCAICIIGIICAAICAIGCGAAACGAICCICAICCIGICIII 3538
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                                                                                                                                                                                                                                                 GAGAACCTGCGAGCAATCCAATCTTCAATCAAGGAAACGATCCTCATCCTGTCTTT
                                                                         781 CGGTCTTGACAAAAAAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,082A

FILING DATE: 13-FEB-1998

CLASSIFICATION NUMBER: US/09/023,082A

PILING DATE: 13-FEB-1998

PILING DATE: 14-FEB-1995

PRIOR APPLICATION NUMBER: US 08/461,195

PRIOR APPLICATION NUMBER: US 08/461,195

PRIOR APPLICATION NUMBER: US 0/023,852

PRIOR APPLICATION NUMBER: US 60/023,852

PRIOR APPLICATION NUMBER: US 60/039,045

PRIOR APPLICATION NUMBER: US 80/039,045

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 80/039,045

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 80/030,045

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 80/030,045

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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APPLICANT SUBEN, STEVEN M.
APPLICANT TURENEZ, PABLO
APPLICANT ADMEN, D. ROXANNE
APPLICANT RAMPY MAKE A.
APPLICANT RAMPY MAKE A.
APPLICANT MENDRICK, DONNA
APPLICANT ZIANG, JUN
APPLICANT ZIANG, JUN
APPLICANT GOLEMAN TIMOTHY A.
APPLICANT OCLEMAN TIMOTHY A.
APPLICANT DILLON, PATRICK J.
APPLICANT DILLON, PATRICK J.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX, P.L.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 147, Application US/09023082A Patent No. 6077692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 2000-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 NEW CITY: WASHINGTON STATE: DC
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.034000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FILEFAX: 202-371-260
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
                                                                                                                                                         1488.0340006
                                                                                                                                                                                                                                                                                                   TYPE: mucleic acid strangers: poth TOPOLOGY: both MOLECULE TYPE: cDNA US-09-044-856A-7
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3359 CGGTCTTGACAAAAAAAAACGGGGGGCGCCTGCGCTGACAGCCGGAACACGGGGGGCATCAG 3418
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                                                                                                                                                                                                 901 GAGAACCIGCGAGCAAICCAICTIGIICAAICAIGCGAAACGAICCICAICCIGICICII
                                                                                     781 CGGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGGCATCAG
                                                                                                                                                                 841 AGCAGCCGATTGTCTGTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09044855A

Patent No. 6100389
GENERAL INPORMATION:
APPLICANT: LI, HADDONG
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A HUMAN CHEMOTACTIC
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
ADDRESSEE: STERNE, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
CITY: WASHINGTON
COTAMES OF SCREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                        3539 GATCAGATCTTGATCCCTGCGCCATCAGATCTTGGCGGC 3579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,855A
FILING DATE: US/09/044,855A
FILING DATE: US/09/044,855A
FILING DATE: US/09/044,855A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: 08/479,126
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTONENTY-AMANTON: PCT-V
NAME: CEMPETE 16-MAY-1994
NAME: CEMPETE 16-MAY-1994
NAME: CEMPETE 16-MAY-1994
NAME: CEMPETE 16-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEPFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERNCE/POCKET NUMBER: 1488.0340005
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3974 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE:
US-09-044-855A-7
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US-09-044-855A-7
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                                                                                                                                                           1488.0360008/EKS
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STBEFEF, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: both
MOLECULE TYPE: cDNA
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                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,670
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
GENERAL INFORMATION:
APPLICANT: OLSEN, HENRIK S.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/046,415
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE DOCKET NUMBER: 1488.093001
TELEPHONE: (202) 371-2600
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 1001; Conservative
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STRANDEDNESS: both
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                                                                                                TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
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                                                                                             1488.0300002
NAME: STEFFE, ERIC K,
REGISTRATION NUMBER: 36,689
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 14;
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
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CGAACAGITTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA
                                                                                                                                                        TCTCGGCAGGAGGAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA
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Patent No. 630338
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NWW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: Herewith
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APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                        TCGAACCCCAGAGTCCCGCTCAGAACTCGTCAAGAGGCGATAGAAGGCGATGCGCT
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Patent No. 6420116
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
TITLE OF INVENTION: Atland.crobial Peptide
FILE REFERENCE: 1488.0930002
CURRENT APPLICATION NUMBER: US/09/627,154
CURRENT FILING DATE: 2000-07-27
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3359 CGGTCTTGACAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAAACACGGCGGCATCAG
                                                                                               3419 AGCAGCGAFTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                GAGAACCTGCGTGCAATCCATCTTGTTCAATGCGAAACGATCCTCATCCTGTCTTT
                                                 841 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DUAN, D. ROXANNE
APPLICANT: SHIATIFARD, ALI
APPLICANT: CONAMAY, JOAN
APPLICANT: CONAMAY, JOAN
TITLE OF INVENTION: ELL2, A New Member of an ELL Family o
TITLE OF INVENTION: RNA POlymerase II Blongation Factors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIF: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: BLORY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/362,871
FILING DATE:
FILING DA
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Pred. No. 0;
; Mismatches
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CCASSIFICATION;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,343
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.08
TELECOMMUNICATION INFORMATION:
TELEFONE (202) 371-2600
TELEFONE: (202) 372-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09362871
Patent No. 6379923
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
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             3419 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG 3478
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Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: vector US-09-027-287-50
                                                                                                                          GAICAGAICTIGAICCCCIGCGCCAICAGAICCIIGGCGGC 1001
                                                                                                                                                        3539 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 3579
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APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Ulden, Stewen M.
TITLE OF INVENTION: Apoptosis Inducing Molecule II
FILLE REPRENCE: 1488,055004
CURRENT PELING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: US 09/003,886
EARLIER APPLICATION NUMBER: US 09/003,886
EARLIER PELING DATE: 1998-01-07
EARLIER PILING DATE: 1996-01-07
EARLIER PILING DATE: 1996-01-07
EARLIER FILING DATE: 1996-03-21
EARLIER FILING DATE: 1996-10-31
EARLIER PELING DATE: 1996-10-31
EARLIER PELING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                        Sequence 50, Application US/09027287A Patent No. 6479254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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US-09-027-287-50
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PRIOR APPLICATION NUMBER: US 09/078,670
PRIOR FILING DATE: 1998-05-14
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 4
LENGTH: 3974
TYPE: DNA
CREANISM: SYNCHETIC CONSTRUCT
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2939 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG 2998
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                                                                                       481 GACCGGCTTCCATCCGAGTACGTGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG
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100.0%; Pred. No. 0;
tive 0; Mismatches 0;
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Patent No. 6495128
Patent No. 6495128
APPLICANT: Salcedo, Theodora W. APPLICANT: Salcedo, Theodora W. APPLICANT: OTHER ROBERT J.B. APPLICANT: OTHER CHEMONINB BETA-7
FILE REFERENCE: 1488.033000F
CURRENT FILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
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Matches 1001; Conservative
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2639 AAGGCGGCGGGAAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGTCATT
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Patent No. 649520
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
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APPLICANT: Coleman, Timothy A.
TITLE OF INVENTION: Expression Control Sequences
FILE REFERENCE: PV447
CURRENT APPLICATION NUMBER: US/09/044,796A
CURRENT FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 08/941,020
PRIOR FILING DATE: 1997-09-30
PRIOR FILING DATE: 1998-03-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 3984
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100.0%; Pred. No. 0;
tive 0; Mismatches
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; Patent No. 6194168
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1001; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
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APPLICANT: Ruben, Steven M.
APPLICANT: Zhang, Jun
APPLICANT: Ullrich, Stephen
APPLICANT: Ullrich, Stephen
TITLE OF INVENTION: Apoptosis Inducing Molecule II and
FILE REPREBENCE: 1488 (055006
CURRENT APPLICATION NUMBER: US/09/252,656B
CURRENT APPLICATION NUMBER: US 60/075,409
PRIOR APPLICATION NUMBER: US 60/075,409
PRIOR APPLICATION NUMBER: US 60/075,409
PRIOR FILING DATE: 1998-02-20
PRIOR FILING DATE: 1998-02-07
PRIOR FILING DATE: 1998-02-07
PRIOR FILING DATE: 1998-03-07
PRIOR FILING DATE: 1998-03-07
PRIOR FILING DATE: 1996-03-1
PRIOR FILING DATE: 1996-03-21
PRIOR APPLICATION NUMBER: US 60/013,923
PRIOR FILING DATE: 1996-03-21
PRIOR APPLICATION NUMBER: US 60/013,923
PRIOR FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 61
SOPTWARE: PatentIn version 3.1
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100.0%; Pred. No. 0;
tive 0; Mismatches
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; OTHER INFORMATION: PHE4-5 expression vector

US-09-252-6568-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 1001, Conservative
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                 2941 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCA 3000
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GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCA 300
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                                                     GCCGGCCACAGTGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
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GREAKAL INFORMATION:
APPLICANT: Fompejus, Markus
APPLICANT: Froger, Burkhard
APPLICANT: Schroeder, Hartwig
APPLICANT: Schroeder, Hartwig
APPLICANT: Action of Regor
APPLICANT: Hacher, Schroeder, Carina
APPLICANT: MARCHER, CALINA
APPLICANT: MARCHER, 109,00201,030
FILE REPERENCE: BG1-123CP
CURRENT FILING DATE: 2000-11-29
CURRENT FILING DATE: 2000-10-30
FRICR APPLICATION NUMBER: 60/142618
FRICR APLICATION NUMBER: 60/142618
FRICR FILING DATE: 1999-06-25
FRICR FILING DATE: 1999-06-25
FRICR FILING DATE: 1999-06-25
FRICR FILING DATE: 1999-07-01
FRICR APPLICATION NUMBER: 60/142690
FRICR APPLICATION NUMBER: 60/142690
FRICR APPLICATION NUMBER: DE 1993-07-01
FRICR APPLICATION NUMBER: DE 1993-07-01
FRICR APPLICATION NUMBER: DE 1993-07-03
FRICR APPLICATION NUMBER: DE 1993-07-03
FRICR APPLICATION NUMBER: DE 1993-07-03
FRICR APPLICATION NUMBER: DE 1993-122.
FRICR APPLICATION NUMBER: DE 1993-122.
FRICR PRICR APPLICATION NUMBER: DE 1993-122.
FRICR PILING DATE: 1999-07-03
FRICR APPLICATION NUMBER: DE 1993-122.
FRICR FILING DATE: 1999-07-09
 US-10-120-398-16
US-10-120-347-16
US-10-120-44-16
US-10-035-212-147
US-09-921-143-16
US-10-08-88-16
US-10-08-488-16
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US-10-05-48-16-147
US-10-261-950-37
US-10-275-446-147
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US-09-897-511A-9
US-10-377-138-13
US-10-377-138-13
US-10-377-138-13
US-10-9921-143-36
US-10-993-11
US-10-993-11
US-10-993-11
US-10-993-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/10307138
Publication No. US20030162267A1
GENERAL INFORMATION:
                                                                 US-10-307-138-14/c
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Sequence 15, Appl
Sequence 50, Appl
Sequence 8, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 12, Appl
                                                                                                    2004, 16:21:35 ; Search time 420.484 Seconds (without alignments) 8769.219 Million cell updates/sec
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                                                                                                                                                                                                         cgctggaggatcatccagcc......gccatcagatccttggcggc 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUG_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
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            version 5.1.6
- 2004 Compugen Ltd.
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US-09-972-912-8

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US-09-973-726-16

US-09-913-726-16

US-09-105-470-25

US-09-105-470-25

US-09-989-687-12

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                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           2449703 seqs, 1841816367 residues
                                                                                                                                                                        US-09-921-143-36_COPY_4000_5000
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                                                                      nucleic search, using sw model
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          GenCore
Copyright (c) 1993
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seq length: 200000000
                                                                                                          February 15,
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Perfect score:
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY: TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY: TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY: TITLE OF INVENTION: BGI-123CP2
CURRENT APPLICATION NUMBER: US/10/307,138
CURRENT FILING DATE: 2002-10-29
PRIOR PELICATION NUMBER: 09/422618
PRIOR PELICATION NUMBER: 06/42618
PRIOR PELICATION NUMBER: 06/141031
PRIOR PELICATION NUMBER: 06/141031
PRIOR PLING DATE: 1999-06-25
PRIOR PELICATION NUMBER: 06/151251
PRIOR PLING DATE: 1999-06-27
PRIOR PELICATION NUMBER: DE 19930476.9
PRIOR PELICATION NUMBER: DE 1993149.5
PRIOR PELICATION NUMBER: DE 19931420.9
PRIOR PELICATION NUMBER: DE 19931420.9
PRIOR PELICATION NUMBER: DE 19931420.9
PRIOR PELICATION NUMBER: DE 1993122.1
PRIOR PELING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 1993122.1
PRIOR PELING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 1993122.1
PRIOR PELING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 1993122.1
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PRIOR APPLICATION NUMBER: DE 1993122.1
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                                                    CGGTCTTGACAAAAAAAACCGGGGGGCGCCTGCGCTGACAGCCGGAACACGGGGGCATCAG
                                                                                CGGTCTTGACAAAAAGAACGGGCCCCCTGCGCTGACAGCGGGAACACGGCGCATCAG
                                                                                                                                                                       550 AGCAGCCGATTGTCTCTTGTCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCC
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                                                                                                                                                                                                                 GAGAACCTGCGTGCAATCCATCTTCAATCATGCGAAACGATCCT
                                                                                                                                                                                                                                                                                                 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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LOCKRION: (457)..(1248)
OTCHRINFORMATION: kanamcyin resistance gene form Tn5
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/10307138 Publication No. US20030162267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kroger, Burkhard
Schroeder, Hartwig
Zelder, Oskar
Haberhaer, Gregor
Haefner, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: vector
OTHER INFORMATION: pINTEGRATIV
                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
COATION: (1515)..(2375)
OTHER INFORMATION: Ori from pMB for replication in E.coli
US-10-307-138-14
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (457)..(1248)
OTHER INFORWATION: kanamycin resistance gene from Tn5
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Batches 1001; Conservative 0; Mismatches
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                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
                                       Q ID NO 14
LENGTH: 2406
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610 CGGTCTTGACAAAAAAAACCGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
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                                                                  GAGAACCTGCGTGCAATCCATCTTGTTCAATCAAACGAAACGATCCTCATCTTGTCTTT
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                                                                                                                                                                     GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                                                                                                              GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 390
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APPLICANT: Enher, Reinhard
APPLICANT: Tu, Guo-Liang
APPLICANT: Tu, Guo-Liang
APPLICANT: Tu, Guo-Liang
APPLICANT: Ullrich, Steven M.
APPLICANT: Ullrich, Stephen
TITLE OF INTERNION: Apoptosis Inducing Molecule II
FILE REPERENCE: 1488.0650004
CURRENT PAPLICATION NUMBER: US 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1997-03-21
EARLIER FILING DATE: 1996-03-21
EARLIER FILING DATE: 1996-03-21
EARLIER FILING DATE: 1996-03-21
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATENTIN VONS: 55
SOFTWARE: PATENTIN VON: 2.0
EBO ID NO 50
EBO ID NO 50
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                               Sequence 50, Application US/09027287A Patent No. US20020064869A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 1001; Conserv
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                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(61)
OTHER INFORMATION: fragment of rxa02910 (cont. from bp 2772 in
OTHER INFORMATION: circular plasmid)
FRANTURE:
NAME/KEY: misc_feature
LOCATION: (2407)..(2772)
OTHER INFORMATION: fragment of rxa02910 (1st part to be con. from bp
OTHER INFORMATION: 1 to 61 in circular plasmid)
                                                                                                                                                                                                                                            DB 13; Length 2772;
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                                    for replication in E.coli
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NAME/KEY: misc feature
LOCATION: (1515)..(2375)
OTHER INFORMATION: Ori from pMB
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US-10-307-138-15
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Matches 1001;
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
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COTHER INFORMATION: pHE4-5 expression vector
US-09-252-656B-50
                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                          PatentIn version 3.1
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
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APPLICANT: Ebner, Steven M.
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Patent No. US202027640A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.L.L.C.
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CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-09-902-684-14
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                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09972912

Patent No. US2002010867A1
GENERAL INFORMATION:
APPLICANT: SOPPET, DANIEL R.
RUBEN, STEVEN M.
TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
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               GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCT
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COMPUTE: DC
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTE: DATE: D-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,912
FILING DATE: 10-OCC-2001
CLASSIFICATION: «Unknown»
APPLICATION NUMBER: 09/049,022
FILING DATE: «Unknown»
APPLICATION NUMBER: 09/049,022
FILING DATE: «Unknown»
ATORNEY/AGENT INFORMATION:
NAMME: STREFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0620001
TELECOMMUNICATION INFORMATION:
MEDITALION NUMBER: 1488.0620001
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-972-912-8
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
Matches 1001; Conserv
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US-09-972-912-8
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          601 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCC
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100.0%; Pred. No. 0;
ive 0; Mismatches
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US-09-935-726-16
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Best Local Similarity 100.
Matches 1001; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
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                                                          APPLICATION UNMER: US/09/902,684
FILING DATE: 12-Jul-2001
CLASSIFICATION CADATO:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/026,408
FILING DATE: AUDMINOWN-
APPLICATION NUMBER: 09/026,408
FILING DATE: 40-AUG-1996
ATTOANSY/AGENT INFORMATION:
NAME: STEFFE, BRIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
92-09-902-684-14
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
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STRANDEDNESS: both
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Best Local Similarity
Matches 1001; Conserv
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
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          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,470
                                   APPLICATION NUMBER: US/09/105, FILING DATE: Herewith CLASSIFICATION: DATA: APPLICATION DATA: APPLICATION DATA: BEING APPLICATION NUMBER: US 60/051, FILING DATE: 27-UNY-1997 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 36,688 REFERENCE/DOCKET NUMBER: 1488. TELECHONICATION INFORMATION: TELECHONICATION INFORMATION INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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US-09-105-470-25
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                                                                                                 2879 GCCGGCCACAGTCGATGATCCAGAAAAGCGGCCATTTTCCACACATGATATTCGGCAAAGC
                                                                                                                                                       AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG
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                                                        GCCGGCCACAGTCGATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
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US-09-105-470-25
US-09-105-470-25
US-09-105-470-25
Sequence 25, Application US/09105470
Publication No. US20030022275A1
GENERAL INFORMATION:
APPLICANT: Carter, Kenneth C.
TITLE OF INVENTION: Human NK-3 Related Prostate Specific TILLE OF INVENTION: Gene-1
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCES: 30
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
COLDSTEIN MASHINGTON
COURT.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
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COUNTRY: US
ZIP: 20005
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                                                                                                                                                                                                                     1488.0360008/EKS
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100.0%; Score 1001; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGBNT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360001
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-371-2600
TELEFAN: 202-371-260
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US-09-345-373-147
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                                               CGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
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1100 NEW YORK AVE, NW, SUITE 600
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-MG-1996
FRICOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-78B-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
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APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-UTN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 147, Application US/09345373
Publication No. US20030077695A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
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DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , STEVEN M.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOORE, PAUL A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WASHINGTON
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2939 AGGCATCGCCATGGGTCACGAGATCCTCGCCGTCGGGCATGCGCCCTTGAGCCTGG 2998
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        361 AGGCATCGCCATGGGTCACGAGGAGCTCCTCGCCGTCGGGCATGCGCCCTTGAGCCTGG 420
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Publication No. US20040002449A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hastings, Greg M.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
FILE REPRESENTS: 1269,107000D
CURRENT APPLICATION NUMBER: US/09/989,687
CURRENT FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
ILENGTH: 3974
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US-09-989-687-12
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    121 TCGAACCCCAGAGTCCCGGTCAGAAGAACTCGTCAAGAAGGCGGTAGAAGGCGATGCGCT 180
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APPLICANT: Irrela-Arispe, Luisa
APPLICANT: Hastings, Gregg A.
APPLICANT: Ruben, Steven M.
APPLICANT: Tonak, Zdenka L.
APPLICANT: Tronak, Zdenka L.
APPLICANT: Tronak, James A.
APPLICANT: Fromwald, James A.
APPLICANT: Fromwald, James A.
APPLICANT: Tronib, Stephen H.
APPLICANT: Tronib, Stephen H.
APPLICANT: Tronaklan A.
TITLE OF INVENTION: Meth. and Meth. Polymucleotides and Polypeptides
FILE REFERENCE: 1468-1070006
CURRENT PELICATION NUMBER: US/09/373,658
CURRENT PILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
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ORGANISM: Homo sapiens
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2879 GCCGGCCACAGACGATGCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 2938
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APPLICANT: Ullrich, Stephen

PEPLICANT: Zhai, Yifan

TITLE OF INVENTION: Approprise Inducing Molecule II and Methods of INTLE REFERENCE: 1488.05000B

FILE REFERENCE: 1488.05000B

CURRENT PELLING NUMBER: US/10/375,680

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,234

PRIOR APPLICATION NUMBER: 2003-01

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 0;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 50
LENGTH: 3974
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Sequence 50, Application US/10375680
Publication No. US20040009147A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M

RESULT 12 US-10-375-680-50

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2759 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTGGCCGCAA 2818
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APPLICANT: Salcedo, Theodora W. APPLICANT: Patel, Vikram, P.
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                                        CGTCTTGACAAAAGAACCGGCGCCCCTGCGCTGACAGCCGGAACAGCGGGGGATAAG
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CGGTCTTGACAAAAAAAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGGGGCATCAG 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Human NK-3 Related Prostate Specific Gene-1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/614,275
FILING DATE: 08-Jul-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                               3539 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 3579
                                                                                                                                                                                                                                                                                                       GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FC
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/105,470B
FILING DATE: 26-Jun-1998
APPLICATION NUMBER: US 60/051,080
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0790001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

S40-10-614-275-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/10614275; Publication No. US20040014668A1; GENERAL INFORMATION:
APPLICANT: Carter, Kenneth C.
He, Wei-Wu
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INFORMATION FOR SEQ ID NO: 25:
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STRANDEDNESS: both
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0520001/EKS/RCM
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON STRATE: DC COUNTRY: USA ZIP: 20005-2934

COUNTRY: USA ZIP: 20005-3934

COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPACIDE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1. APPLICATION DATE: 19-011-2002

CURRENT APPLICATION AUMBER: US/09/015,963

FILING DATE: 401ACOMMAN PRELICATION NUMBER: US/09/015,963

ATTORNEY, AGENT THORDAMION: NUMBER: US/09/015,963

ATTORNEY, AGENT THORDAMION: WARNEY, US/000101 PROCESSEE FOR AUTOMAN PARTORNEY, AUGUST AUTOMAN PARTORNEY, AUMBER: US/000101 PROCESSEE PATORNEY, AUGUST AUTOMAN PARTORNEY, AUTOMAN PARTORNEY, AUTOMAN PARTORNEY, AUGUST AUTOMAN PARTORNEY, AUMBER: US/00010 PATORNEY, AUTOMAN PARTORNEY, AUTOMAN PART
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-197-844-9
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02) 371-2540
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) Publication No. US20031066898A1
GENERAL INFORMATION:

APPLICANT: CHOPRA, ARVIND
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GENTZ, REINER
RUBIN, STEVEN M.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE,
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STRANDEDNESS: both
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US-10-197-844-9
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               APPLICANT: Graham, Gerard J.
TITLE OF INVENTION: CHEMOKINE BETA-7
FILE REFRENCE: 1488.033000F
CURRENT APPLICATION NUMBER: US/10/260,270
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US/09/437,602
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
Nibbs, Robert J.B.
                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-260-270-4
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Search completed: February 15, 2004, 22:26:53 Job time : 425.484 secs

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COMMENT
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AQ447775 mgxb0011B
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop_60.0 , Gapext 60.0
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AQ448898 mgxb0022E
AQ44387 V107H5 mT
BH91221 PST277.8e
AQ874213 V104H2 mT
AQ87288 V1054F2 mT
AQ389385 mgxb00100
AQ84178 V104C5 mT
AQ361943 mgxb0005M
BM056700 2107-31 h
AQ873679 V73F2 mTh
AQ876036 V132E1 mTh
AQ876036 V132E1 mTh
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Saccharomyces cerevisiae
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetels;
Saccharomycetales;
Saccharomyces
Saccharomyces.

I (bases 1 to 784)
Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Gestages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQB76152 184 bp DNA linear GSS 08-NOV-1999 V133H12 mIn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces carevisiae genomic 5', genomic survey sequence.
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V130H11 m
V120D2 mT
V61A6 mTn
V133F5 mT
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V120E4 mT
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P.O. Box 208103, New Haven, CT 06520-8103, USA
FIL: 203 432 949
Fax: 203 432 516
Email: anuj.kumar@yale.edu
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KEYWORDS
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GSS.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Eukäryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (baese 1 to 85. A., Cheung, K.-H., Sheehan, A., Saroniatis, D., Jansen, R., Umansky, L., Heidtman, M., Saroniatis, D., Jansen, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M., Ranada, D., Lugo, R., Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain Y2278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="wTn-3xHA/lacz Insertion Library, strain Y2278'
/note="Vector: pH885-8al, A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pH886-8al; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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/lab_host="E. coli"
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Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
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Best Local Similarity 100.0%; Pred. No. 5.7e-287;
Matches 568; Conservative 0; Mismatches 0;
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te of mfn-3xEA/lacZ insertion.
Seq primer: GGCCTTCTTTTGGAAGTAC
Class: transposon-tagged.
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          KEYWORDS
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                                                                                                                                                                                                  /clone_lib="mrn-3xHA/lacz Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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/strain="Y2278 - 2288C background, cir(0) rho(0)"
/db xref="taxon:4932"
/lab_host="E. coli"
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100.0%; Pred. No. 5.6e-287;
ive 0; Mismatches 0;
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te of mTn-3xHA/lacz insertion.
Seq primer: GGCCTTCTTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
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MGXA0011E13f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0011E13f, genomic survey sequence.

AQ447775
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Rice blast is one of the most devestating fungal diseases
                                                                                                                                                                                                                                                                                              GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCA 493
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Magnaporthe grisea
Bukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

[ (bases 1 to 509)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                       GCCGGCCACAGAGGGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
               TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                      314 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGAAGGCGATAGAAGGCGGTGCGCT
                                                                                                                               GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGGAAGCGGTCAGCCCATTCGCCGCCAA
                                                                                                                                                                                     374 GCGAATCGGGAGGGGGGGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tal: 864 655 5737
Fax: 864 656 4293
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/strain="70-15"
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geg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 342.
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Saccharomyces cerevisiae
Bukaryota; Pungi; Ascomycota; Saccharomycetes;
Bukaryota; Pungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomyces.

I (bases 1 to 798)
Stoss-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Gestlages, S.A., Cheung, K., Iwasaki, H., Kanada, D., Jugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
L Umpublished
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
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/mol_type="genomic DNA"

/strain="Y2278 - S288C background, cir(0) rho(0)"

/db xref="taxon.4932"

/lab host="E. coli"

/lab host="E. coli"

/clone_lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"

/clone_lib="mTn-3xHA/lacZ Insertion Library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance.
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                               CGAACAGTTCGGCTGGCGCGCGCGCCCCTGATGCTCTTCGTCCAGATCCTGATCGACAA
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/organism="Saccharomyces cerevisiae"
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Pred. No. 9.3e-262;
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te of mTn-3xHA/lacZ insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
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/clone_lib="min-3xHA/lacz Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="yellow and proceed of the pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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BAC Library Magnaporthe grisea genomic
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/db_xref="taxon:4932"
/lab_host="E. coli"
               Kumar A
Snyder, Dept. of Mol. Cell. and Dev. Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 790;
 Contact: Kumar A
Michael Snyder, Dept. of Mol. Cerr.
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 9161
Email: anuj. kumargyale.edu
te of min-3xHA/lacZ insertion.
Seg primer: GGCTTCTTTTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
Location/Qualifiers
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Pred. No. 1.9e-255;
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GSS.

Saccharomyces cerevisiae (baker's yeast)

Saccharomyces cerevisiae

Sucaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomycetes;

Saccharomycetales; Saccharomycetales; Saccharomyces.

Labses 1 to 790)

Roses Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Geste ages, S., Cheung, K.-H., Sheelan, A., Swmoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Distription
of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Vl32H11 mTn-3xHA/lacZ Insertion Library, strain
cerevisiae genomic 5', genomic survey sequence.
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Pred. No. 1.8e-255;
0; Mismatches 0;
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100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 655 737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 422.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="70-15"
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/Lissue Lype="Protoplasts"
/Lissue Lype="Protoplasts"
/Lisb_host="E_coli DH10B"
/Colne_lib="Cugi Rice Blast BAC Library"
/note="Vector: pB4CWICH; Site 1: HindIII; Site 2: HindIII;
/Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction.
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
/kbp was constructed. This library represents greater
than 25% genome coverage. High density colony filters
are available upon request. " 3 others
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                                                                                                                                                                              1 (bases 1 to 789)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                                                    Bukaryota, Fungi, Ascomycota; Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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                                                                                                                                                                                                                                                                                                                   Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tal: 864 655 5737
Fax: 864 656 4293
                                                                                        Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
  clone mgxb0005K01f, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Magnaporthe grisea"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC enda
High quality sequence start: 41
High quality sequence stop: 392.
Location/Qualiflers
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/clone="mgxb0005K01f"
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/strain="70-15"
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Magnaporthe grisea
Bukaryota; Fungi Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incerteae sedis; Magnaporthaceae; Magnaporthe.

(bases 1 to 499)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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/tissue_type="Totoplasts"
/lissue_type="Totoplasts"
/lab host="E coil DH:08"
/clone_lib=cucil Rice Blast BAC Library"
/clone_lib=cucil Rice Blast BAC Library
/clone world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome with an average insert size of 130
/kbp was constructed. This library represents greater
than 25% genome coverage. High density colony filters
are available upon request."
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mgxb0006009f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0006009f, genomic survey sequence.
AQ447230.1 GI:4576367
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                                                  49.9%; Score 499; DB 28; I
100.0%; Pred. No. 9.6e-251;
ive 0; Mismatches 0;
                               /db xref="taxon:148305"
/clone="mgxb0023E21f"
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Matches 499;
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                        ACCAGGCCGCCACAGTCGATGAATCCAGAAAAGCGCCATTTTCCACATGATATTCGG
                                                                                                           GCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAAGAAGCGGTCAGCCCATTCGCC
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Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Dean RA
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Oordan Hall, Clemson University, Clemson, SC 29634
Tal: 864 656 4293
         Length 499;
                                       Indels
                         9.3e-251;
       DB 28;
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/mol_type="genomic DNA"
49.9%; Score 499; DB
llarity 100.0%; Pred. No. 9.3
Conservative 0; Mismatches
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 395.
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GSS.
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                   al Similarity
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DEFINITION
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AQ449162/c
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AUTHORS
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VI20E4 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Buckaryota, Fungi; Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 81)
Rosse Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Jansen, R., Umansky, L., Miller, P., Roeder, G.S. and Snyder, M.

Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

Gene Disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="mtn-3xHA/lacz Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
was prepared in
pHSS6-Sal; genomic DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mtn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT 180
                                                                                                                                           64 TCAGCCATGATACTTTCTCGGCAGGAAGGAAGGTGAGATGACAGGAGATCCTGCCC
                                              124 TTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCAGCCGCATTGCA
                                                                                                       582 TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCC
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         /mol_type="genomic DNA"
farrain="12278 - S288C background, cir(0) rho(0)"
/db xref="taxon:4932"
/lab_host="E. coli"
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Michael Snyder, Dept. of Mol. Cell. and Dev. Bi
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
P.D. 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Saccharomyces cerevisiae"
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100.0%; Pred. No. 1.4e-247;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: anuj.kumar@yale.edu
Le of mTh.3XHA/LaZ insertion.
Seq primer: GGCCTTCTTTTGGAAGTAC
Class: transposon-tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /done lib="CUGI Kice Black BAC Library" / clone lib="CUGI Kice Black BAC Library" / note="Wector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice Black is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal lost interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request." I others
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                          Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                                                                                             Contact: Dean RA
Clemson University Genomics Institute
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 4293
Email: rdeamolaemson.edu
Seq primer: TAATACGACTATAGGG
Class: BAC ends
High quality sequence stop: 291.
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mol_type="genomic DNA"
strain="70-15"
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/clone="mgxb0006009f"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
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AQ875907 801 bp DNA linear GSS 08-NOV-1999 V130H3 mIn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Baccharomycetales; Saccharomycetaceae; Saccharomyces.

[ (bases 1 to 801)
Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
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Michael Snyder, Dept. of Mol. Cell. and Dev.
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, US
Tel: 203 432 9949
Fax: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTTGGAAGTAC
                                                                     Score 489, DB 28, I Fred. No. 1.8e-245;
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                                                                   Query Match
48.9%; Score 489; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 489; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Saccharomyces cerevisiae"
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/strain="Y228" - $288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
/dab_host="E. coli"
/lab_host="E. coli"
/clone_llb="mn-3xHa/lacZ Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mrn-3xHa/lacz
minitransposon containing lacz, URA3, and tet resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ876220 1799 bp DNA linear GSS 08-NOV-1999 VIS2G7 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
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                                                                                              GCGAATCGGGGGGGGGTATCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA 454
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                     TCGAACCCCAGAGTCCCGCTCAGAAGACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                           GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCCATTCGCCGCCAA
                                                                                                                                         GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCA
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Saccharomyces cerevisiae
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te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
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Location/Qualifiers
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AQ876220.1 GI:6288464
GSS.
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desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Tunsen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Miller, P., Roeder, G.S. and Snyder, M. Gene Disruption
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100.0%; Pred. No. 3.2e-240;
ive 0; Mismatches 0;
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                                                                                                                                     Contract: Kumar A
Michael Snyder, Dept. of Mol. Cell. a
Yale University
P.O. Box 208103, New Haven, CT 06520-
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mIn-3xHA/lac2 insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
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Class: transposon-tagged
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                                                                 /organism="Saccharomyces cerevisiae"
/mol type="genomic DNA"
/strain="12726 - 8288C background, cir(0) rho(0)"
/strain="12726 - 8288C background, cir(0) rho(0)"
/db xref="taxon:4932"
/lab host="E. col!"
/clone_lib="mtn-3xHA/lacZ Insertion Library, strain Y2278"
/note="Vector: pRSS6-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mtn-3xHA/lacZ
minitransposon containing lacz, URA3, and tet resistance.
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V132C9 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 783)
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Pred. No. 2.9e-241;
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                            transposon-tagged.
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/lab_host="E. coli DH10B"
/clone lib="CGI Rice Blast BAC Library"
/clone lib="CGI Rice Blast BAC Library"
/note="Vector: pBACMICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous assomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of the kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request. 12 others
                       AQ447874 SSS 08-APR-1999 MAXD0012101f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0012101f, genomic survey sequence.
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Magnaporthe grisea
Bukaryota, Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

[ bases 1 to 561)
Yu.Y. Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Contact: Dean RA
Clemson University Genomics Institute
Clemson University
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TATARGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 42
High quality sequence start: 42
High quality sequence stop: 326.
Location/Qualifiers
1. 561
Jordanian="Manaporthe grisea"
//etrain="Manaporthe grisea"
//etrain="Manaporthe grisea"
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/tissue types = Proplasts"

/lab hose="E. coli DH10B"

/clool 11b="CG1 ENGISTE BAC Library"

/clool 11b="CG1 ENGISTE BAC Library"

/note="Vector: pBA7MICH; Site 1: HindIII; Site 2: HindIII;

Rice blast is one of the most devestating fungal diseases

of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
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Magnaporthe grisea
Bukarnota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incerea sedis; Magnaporthaceae; Magnaporthe.

(bases 1 to 620)
Yu, Y. Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Saainowski, M. Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
261 GATACTITCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCTTCGCCC
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 655 4293
Email: rdean@clemson.edu
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100.0%; Pred. No. 1.9e-234;
Live 0; Mismatches 0;
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Clemson University Genomics Institute
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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468 TTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCACACCCACGCG 409
                                                     305 GCCACAGAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGCAAGCAGGG 364
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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E C	BD270607	AK381510 BD001745	BD134149	BC035212 AR231261	AR342826	AR231262	AR342827	AR112510 AR157589	BD247178	AR212635	AR430033 AX234371	AX743106	HSVEGFC	HSU43142 BD247192	HSU58111	BD270608	AB004275		MMU73620		AR212641	AR430039	AR157586	AY032729		AR112512	AR201988 BD082161	AC093801	AF466147	AC140905 AF009178	ALIGNMENTS	1674 bp DNA	raccor	Chordata; Craniata; Ver Primates; Catarrhini; H	der,R., Rosc factor 2 -NOV-2002;
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HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002539082-A/1
PD 19-NOV-2002
PF 07-FEB-2000 JP 2000596954
PF 07-FEB-1999 US 60/119179,12-FEB-1999 US 60/119926 PR 03-JUN-1999 US 60/137795,22-DEC-1999 US 60/17505 PI CRAIG A ROSEN, RALPH ALDERSON, ROBERT MELDER, VIKTOR ROSCHKE, PI STEVEN M RUBEN
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Key
Cost (12.6)

Selg_peptide (12). (80)

mat_peptide (81). (1268).

Location/Qualifiers

1..1674

//organism="Homo sapiens"

//mol_type="genomic DNA"

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Best Local Similarity 100.
Matches 1674; Conservative
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Homo sapiens (human)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
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E 1 (bases 1 to 1674)
AS Rosen, C., Hu, J.-S. and Cao, L.
AL Patent: US 6608182-A 1 19-AUG-2003;
AES 1. 1674
Nource | /organism="unknown" /mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1674; Conservative 0; Mismatches
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DN J0202505873-A/1

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PP 10-MAR-1999 UP 2000535731

PR 13-MAR-1999 UP 2000535731

PR 13-MAR-1999 UP 2000535731

PR 13-MAR-1999 UP 2000535731

PR 13-MAR-1999 US 09/042105, 30-JUN-1998 US 09/107997 PI

CRAIGA ROSBN, LIANG KAO, JIN SHAN FU

PC C12N1/21, A61K38/22, A61K48/00, A61P9/10, A61P9/12, A61P17/06, PC

A61P19/02,

PC C07K14/50, C07K16/22, C12N5/10, C12N15/09, C12Q1/68, C12Q1/70, PC

A61K37/24,

PC C12N5/00, C12N15/00

CC Strandedness: Double;

CC Topology: Linear;

CC Vascular endothelial growth factor 2

FH Key

PT Sig_peptide 12.80

FT mat_peptide 12.80

FT CDS

            PAT 18-SEP-2002
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BD134149
N Vascular endothelial growth factor 2.
BD134149.1 GI:23229094
JF 2002505873-A/1.
Unidentified
Unidentified
Unidentified
Unclassified.1 (Dases I to 1674)
Rosen, C.A., Kao, L. and Fu, J.S.
Vascular endothelial growth factor 2
Patent: JP 2002505873-A 1 26-FEB-2002;
HUMAN GENOME SCIENCES INC
OS Unidentified
PN JP 2002505873-A/1
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100.0%; Score 1674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1674; Conservative 0; Mismatches
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DENITCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLKGKKFHQCTGSCYRRPCTNRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/tissue type="Skin, squamous cell carcinoma"
/clone_lib="MGI CGAP_Skn4"
/lab host="DH10B"
/note="Uvector: pCWV-SPORT6.1"
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/note="PDGF; Region: Platelet-derived
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/organism="Homo sapier
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                  gene="VEGFC"
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Matches 1669; Conservative
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Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

Strausberg, R.D., Pelngold, E.A., Grouse, L.H., Derge, J.G.

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatcherko, L., Marusina, K. P., Pordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatcherko, L., Marusina, K., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Stepleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Abrange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Malek, J.A., Gunaratne, P.H., Richads, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Kazywinski, M.I., Skalska, U., Sanilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human, and monre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC035212 1948 bp mRNA linear PRI 07-CCT-2003 Homo sapiens vascular endothelial growth factor C, mRNA (cDNA clone MGC:24887 IMAGE:4753457), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19924300. Location/Qualifiers
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Submitted (31-UUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                              1561 ATTCATTTTTATAGCAACAATTGGTAAAACTCACTGTGATCAATATTTTATATCAT
                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                             BC035212.1 GI:23273809
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JOURNAL
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1111 TAGGAGGAAGTTCATTCCATTATTAGACGTTCCTGGCAGCAACACTACCAC 711 AGCAGGGAACAAGTTCATTCCATTATTAGACGTTCCTGGCAGCAACACACTACCAC 711 AGCAGGGAACAAGACTGCACCCACCAATTACATGGGAATAATCAATTGGTTCTGGAATTAATCATTTGGTTTTATAGATTTTATCTTTTATCTTTTACATGTGGAATTAATCAATTGGATTG	DEFINITION Sequence 1 from patent US 6576608. ACCESSION AR342826.1 GI:33738052 VERSION AR342826.1 GI:33738052 SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (Bases 1 to 2031) AUTHOR Lee, J. and Wood, W. TITLE Methods of using VEGF-related protein JOURNAL Patent: US 6576608-A 1 10-JUN-2003; FEATURES 1. 2031 ACCESSION AR342826.1 GI:3031 AUTHORS Lee, J. and Wood, W. TITLE Methods of Location Journalifiers Location/Qualifiers ACCESSION AR342826.1 GI:3031 ACC	Query Match 99.4%; Score 1664.6; DB 6; Length 2031; Best Local Similarity 99.8%; Pred. No. 0; No. 0; Matches 1667; Conservative 0; Mismatches 4; Indels 0; QY 1 GTCCTTCCACCATGACTCGTGGGCTTCTTCTTCTGTGGCGTGTTCTTCTGCTGCT		AGGAGGAGTTA.CGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT		QY 421 GTATAGATGTGGGGAAGGAGTTTGGAGTACCACCATCTTAAACCTCCATGTG 480 Db 781 GTATAGATGTGGGGAGTTTGGAGTTGCGCGACAAACCACCTTCTTTAAACCTCCATGTG 840 QY 481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCATGAACACCA 540 Db 841 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCATGCA	Oy 541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCTCTCTCT	661 TTTACAGACAAGTTCCATTATTACACGTTCCTGCCAGCAACACTACCACAGTGTC 1021 TTTACAGACAACATCCATTATTACACGTTCCTGCCAGCAACCTACCACAGTGTC 721 AGGAGCGAACAAACCTGCCCCAACTTACATGTGGAATAATCACATTTCACATGTCC	Db 1081 AGGCAGCGAACTACCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 1140
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Alusher, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Saares, M.B., Bondldo, M.F., Casavant, T.L.,
Scheefz, T.E., Brownstan, M.J., Usdin, T.B., Toshiyuki, S.,
Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, B., Retteman, M., Madan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Butterfield, M. Sodergren, E.M., Sono, Ford, Schein, J.B.,
Generation and initial analysis of more than 15,000 full-length
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Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Bletrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskelllo,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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TEETIKFAAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKBFGVATNTFFKPPCVSVY
RCGCCCNSEGLQCMYTSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVY
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19924300.
Location/Qualifiers
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/organism="Homo sapiens"

/organism="Homo sapiens"

/mol_type="mrMa"

/db_xref="teaxon:9606"

/clone="MGC:74703 IMAGE:4513834"

/clone="MGC:74703 IMAGE: transitional cell papilloma"

/clone="lb="NIH MGC_93"

/lab hos=="DH10B"

/note="Vector: pCMV-SPORT6"
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Contact: MgC help desk
Email: cgapbs-ramail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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AUTHORS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           1141 TGGCTCAGGAAGATTTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
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KACEPDFSYSEEVCRCVPSYWRRPQMS"
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              651 ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
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Lee,J. and Wood,W.
Methods of using VEGF-related protein
Patent: US 6576608-A 2 10-JUN-2003;
Location/Qualifiers
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1661 TGCCACAGTAGAACTGTGGACACAGTGGGACCCTTGTGGGTCCATGCTAACAAAGACA 1720 Qy	RESULT 15 AR212635 LOCUS DEPTINITION Sequence 32 from patent US 6403088. ACCESSION AR212635 VERSION AR212635. GI:23309413 KEYWORDS ONCE ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE ALIDAGES RESETTINGER 1 (bases 1 to 1997) AUTHORS Alitalo, K. and Joukov, V. TITLE ALIDAGES RESETTINGER 23 11-JUN-2002; FEATURES LOCATION/QUalifiers LOCATION/Qualifiers OUTHORS AND AND PATENTIA LOCATION/QUALIFIERS LOCATION/QUALIFIERS LOCATION/QUALIFIERS LOCATION/QUALIFIERS AND	ORIGIN Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1653; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 167 CTTCCACCATGCACTGGGGTTCTTCTCTGGGGGTGTTCTCTGCTGGCGGTG 0 GTCCTTCCACCATGCACTTGCTGGGGTTCTTCTTCTGTGGGGTGTTCTTGTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises administering (VEGF-2).
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peripheral arterial disease; critical limb ischaemia; coronary disease;
angiogeneeis; tumour; inflammation; diabetic retinopathy; psoriasis;
rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
infectious disease; neurodegeneration;
vascular endothelial growth factor-B; VEGF-B; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vascular endothelial growth factor 2; VEGF-2; gene; ss; pVGI.1; chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; allergic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferative disorder; viral infection; bacterial infection; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischemia or myocardial ischemia, autoimmune disorders and allergic conditions.
ATTCATTTTTATAGGAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
                                                                 1561 ATTCATTTTTATAGCAACAACAATTGGTAAACTCACTGTGATCAATATTTTTATATCAT
                                                                                                                                                  501 A; 383 C; 376 G; 414 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA.
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Length 1674;

DB 6;

100.0%; Score 1674;

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(HUMA-) HUMAN GENOME SCI INC.

Wager RE; Rosen CA, Albert VR, Ruben SM,

2003-092991/08.

P-PSDB; ABJ19819

New isolated polynucleotide encoding an antibody which inhibits a VEGF-2 polypeptide, useful for diagnosing, treating or preventing diseases associated with aberrant VEGF-2 expression or function, e.g. cancer or inflammation.

Disclosure; Fig 1; 425pp; English.

The invention relates to an isolated polymucleotide encoding a first antibody at least 95-100% identical to a second antibody comprising an amino acid sequence selected from at least one, two or three CDR region(8) of a VH or VL domain where the first antibody is a VEGF-2 polymetric two or three CDR immunospecifically inhibits a VEGF-2 polymetric. The isolated polymucleotide is useful in diagnosing, treating preventing, prognosing, aneliorating or monitoring diseases associated with aberrant VEGF-2 or VEGF-2 or

Sequence 1674 BP; 501 A; 383 C; 376 G; 414 T; 0 U; 0 Other;

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1020 1200 1440 961 GTGTCTGTAAAAACTAAAACTCTTCCCCAGCCAATGTGGGGGCCAACCGAGAATTTGATGAAA 1020 ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCAGAAATCAACCCCTAAATCCTGGAA 1080 1021 ACACATGCCAGTGTGTATGTAAAGAACCTGCCCAGAAATCAACCCCTAAATCCTGGAA 1080 1081 AATGTGCCTGTGAAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGGAAGTTCC 1140 1081 AATGTGCCTGTGAATGTACAGAAAGTCCACAAAATGCTTGTTAAAAGGAAAGAAGTTCC 1140 1440 1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC 1500 1501 TTGTGATTTCTTTAAAGAATGACTATATAATTTTTTTCCACTAAAATATTTGTTTCTGC 1560 1561 ATTCATTTTTATAGCAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT 1620 720 960 481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 540 541 GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTTCTCAAGGCCCCA 600 660 999 720 780 780 840 840 900 841 ÁrGÁCÁTOTGTGGÁCGÁÁACÁÁGGÁGCTGGÁTGÁAGAGAGACCTGTCAGTGTGTCTGCAGAG 900 481 rerecercracadareresegrifectecialaberesegetiscaseresegricareae 901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAGAACTAGACAGAAACTCATGCCAGT **AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG** AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTTAAACTGGATG TITACAGACAAGTICATICCATTATIAGACGTICCCIGCCAGCAACACTACCACAGIGIC 661 TTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACTAGTGTC AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 781 resercaceaacaririrarerriricerecearecregacareaereaereaearece <u>ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG</u> GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA 1141 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAAACCGCCAGAAGGCTTGTGAGC 1201 CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC 1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT 1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTTCTATTATGGAAAACTGTGT TGCCACAGTAGAACTGTCTGTGAACAGAGACACCCTTGTGGGTCCATGCTAACAAAGACA 1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG 1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGTCATCTG 1501 TTGTGATTTCTTTAAAAGAATGACTATATAATTTTATTCCACTAAAAATATTTGTTCC TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 901 cesescrircescrieccaecreresaceccaeaaaaaaacrasaaaaacrearer ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC 1201 CAGGATTITICATATAGIGAAGAGIGIGIGIGIGIGIGICCCTICATATIGGCAAAGACCAC 1321 receacaciaesacrereresacaesacaesecerreresecerecerecrasesacaes 1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC 601 661 721 601 721 781 841 1141 1021 1321 961 d a g g 쉱 à ò à 셤 ઠ d 8 쉱 ò g à Ωp ò g ð 쉱 ò g 8 g ઠે 유 ò ð g ठे g ò ò ò

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This invention describes a novel isolated polymuclectide encoding a first antibody comprising an amino acid sequence selected from at least one, two or three complementarity determining (CBT) region(s) of a VH and/or VL domain of a second antibody that immunospecifically binds to a vascular endothelial growth factor (VBGF)-2 polypeptide. The products of the invention have cytostatic, cardiovascular, antirhemmatic, vulnerary, antializergic immunosuppressive, dermatological, antipalerary, antializergic immunosuppressive, dermatological and antipsoriatic activity. The polymuclectide is useful in diagnosing, treating, preventing, prognosing, ameliorating or monitoring diseases alloger-2 or VBGF-2 or VBGF-2 receptor function, such as cancer and other products (CBCF-2 or VBGF-2 or VBGF-2 receptor function, such as cancer and other products diseases, autoimmune diseases (e.g. rheumatoid arthritis, or proliferative diseases, autoimmune diseases (e.g. rheumatoid arthritis, systemic Lupus Brythematosus, allergies), diabetic retinopathy or the invention may also be used to simulate angiogenesis, wound healing, and promoting vascular tissue repair. The polymuclectide and polypeptide may also be used to simulate angiogenesis, wound healing, may also be used for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors and for the production of diagnostics and therapeutics e.g. one therapy and in vaccines to treat
                           1561 Afficatititiatagcaacaacaarrggraaaacrcacrgrgarcaararrrrarararcar 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic; antiartitic; antidabetic; ophthalmological; antiallergic; vulnerary; immunosuppressive; dermacological; antipsoriatic; proliferative disorder; cancer; cardiovascular disorder; arrhythmia; cerebrovascular disorder; cerebral anoxia; inflammatory disease; infectious disease; anglogenes; autoimmune disease; Systemic Lupus Erythematosus; wound healing; vascular tissue repair; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide encoding an antibody which inhibits vascular endothelial growth factor (VEGF)-2 polypeptide, useful for diagnosing or treating diseases associated with aberrant VEGF-2 expression or function,
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; VH domain; VL domain; vascular endothelial growth factor; VEGF-2;
                                                                        Rosen CA, Albert VR, Ruben SM, Wager RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1A-B; 344pp; English.
                                                                                                                                                                                                                                   ABQ76966 standard; cDNA; 1674 BP.
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                                                                                                                                                                                                                                                                                                                                                                          Human VEGF-2 cDNA SEQ ID 1.
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human diseases. This sequence encodes a polypeptide described in the disclosure of the invention
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0
                                                                                 100.0%; Score 1674; DB 7; Length 1674; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0;
                                                   Seguence 1674 BP; 501 A; 383 C; 376 G; 414 T; 0 U; 0 Other;
                                                                                                    Best Local Similarity 100. Matches 1674; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human vascular endothelial growth factor (VEGF-2) cDNA.
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/product= "Human VEGP-2 protein"
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The invention relates to vascular endothelial growth factor (VEGF)-2 antibodies are useful for treating, preventing or ameliorating a disease or disorder, such as inflammatory diseases or disorders, tumour tumour unetastasis, breast cancer, proliferative disorders, tumour unetastasis, breast cancer, brain cancer, prostate cancer, colon cancer, lymphangioma, an infectious disease, Kapoai's sarcoma, an autoimmune diseases, rheumatoid arthitis, psoriasis, diabetic retinopathy, a disease or disorder associated with aberrant VEGF-2 (receptor) expression, or a disease or disorder antibody is also useful for detecting, diagnosing, prognosing, or monitoring cancers and other hyperproliferative disorders. VEGF-2 is also used in gene therapy. The present sequence is human VEGF-2 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCTGCTCCCGGGTCCTCGCGAGGCGCCCGCCGCCGCCGCCTTCGAGTCCGGACTCG
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Best Local Similarity 100.0%; Score 1674; DB 7; Length 1674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1674; Conservative 0; Mismatches 0; Indels 0;
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                                   /product= "Human mature VEGF-2 protein"
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                                                                                                                                                                                                                                                                                   Albert VR, Ruben SM,
                                                                                                                                                12-APR-2002; 2002WO-US011404;
                                                                                                                                                                                    13-APR-2001; 2001US-0283391P.
07-SEP-2001; 2001US-0317600P.
                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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                                                                         WO200283849-A2
                                                                                                             24-OCT-2002.
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421 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG 480	421 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAACACCTTCTTTAAACCTCCATGTG 480	481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGTGCAGTGCAGTGAACACCA 540	GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCT	601 AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCGATGCATGTCTAAACTGGATG 660 	661 TITACAGACAAGTICCITCCATTATTAGACGTICCCTGCCAGACACACTACCACAGTGTC 720 	721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780 	781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840	841 ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGACCTGTCAGTGTGTCTGCAGAG 900	901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAAACTCATGCCAGT 960	961 GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAAA 1020 	1021 ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCTAAATCCTGGAA 1080 	1081 AATGTGCCTGTGAATGTACAGAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC 1140 1081 AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC 1140	1141 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACGCCAGAAGGCTTGTGAGC 1200	1201 CAGGATTTTCATATAGTGAAGAAGTGTGGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC 1260 	1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAACTGTGT 1320 	1321 TGCCACAGTAGAACTGTCTGTAACAGAGACCCTTGTGGGTCCATGCTAACAAGACA 1380 1321 TGCCACAGTAGAACTGTCTGTGAACAGAGACCCTTGTGGGTCCATGCTAACAAGACA 1380	1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCGTCTG 1440	1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTCCTC 1500 	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ar endothelial growth factor 2 - used to promote alisation in vascular graft surgery.
                                                                                                                                             th factor 2; VEGF2; angiogenesis;
nary bypass surgery; vascular graft surgery;
; therapy; diagnosis; ds.
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                                                                                                                                                                                                                                                                                            protein similar to vascular endothelial growth factor - used to e.g. wounds, tumours, rheumatoid arthritis, Kaposi's sarcoma etc.
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1921 ATTCATTTTTATAGCAACAATTGGTAAACTCACTGTGATCAATATTTTTATATCAT 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; human; vascular endothelial growth factor receptor-3; ligand; angiogenesis; wound healing; lymph vessel; lymphangioma; cancer; metastasis; therapy; diagnosis; plasmid pFLT-4-L; ss.
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                                                                   Human Flt4 receptor tyrosine kinase ligand VEGF-C cDNA
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The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopoiesis. The products can be used for stimulating angiogeneses, for inhibiting angiogenesis, for stimulating lymphangiogenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Mirroy's disease. They can also be used for modulating the growth of endothelial cells. They can also be used for modulating the growth of endothelial cells. They can also be used for stimulate lymphocyte production and maturation, and to promote or inhibit trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus
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AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
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                                                                                                      AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
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                                                                                                          re-endothelialisation;
                                                                                                       Vascular endothelial growth factor-C; VBGF; human; re-endothelialisation; vascular endothelial growth factor receptor; VBGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restenosis agent; prevention; restenosis; stenosis; percutaneous transluminal coronary angioplasty; ss.
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/note= "Encodes carboxy terminal peptide, which on
cleavage results in partially-processed VEGF-C protein"
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                                                                                                                                                                                                                                                                                                                                                                                                 product= "Human prepro-VEGF-C protein"
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                                                      Human vascular endothelial growth factor (VEGF)-C cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preventing stenosis and restenosis in growth factor proteins or the nucleic
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P-PSDB; AAY70982.
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Sequence 1997 BP; 526 A; 527 C; 490 G; 454 T; 0 U; 0 Other; Query Match Best Local Similarity 99.3%; Pred. No. 0; Matches 1653; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Matches 1653; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Additional Conservational Conservation Conservati	401 CGCTGCCGGGTCCTCGCGAAGGCCCCGCCGCCGCCGCCGCCTTCGAGTCCGAACTCG 460 121 ACCTCTCGGACGCGAAGCCGACGCGGCGCCGCCCTTCGAGTCCGAACTCG 180 461 ACCTCTCGGACGCGAAGCCCGACGGGGGGTTATGCAAGCAA	ATTGGAAAATGTACAAGTGTCAAGGAAAGGAGGGGGCTGGCAACATAACAGA CCAACCTCAACTCAA	761 GTATAGATGTGGGGAAGATTTGGAGTCGCGACAAACACTTCTTTAAACCTCCATGTG 820 481 TGTCCGTCTACAGATGTGGGGGGTTTGCTACAGATGGGGGGCTGCATGAGCCTCCATGTG 820 481 TGTCCGTCTACAGATGTGGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 540		ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAACCTGTCAGTGTGTCTGCAGAG 90

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                                                                                                                                            Screening a human subject for increased risk of developing a lymphatic disorder, comprises assaying a nucleic acid to determine a mutation altering the sequence of a vascular endothelial growth factor receptor-3.
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                                                                                                                                                                                                                                                    The present sequence is the coding sequence for the human vascular endothelial growth factor C (VEGF-C). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) allelss they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome, which is early onset lymphoedema and lymphoedema praecox, which is late
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for screening a human subject for an increased risk of developing a lymphatic disorder e.g. hereditary lymphedoema. The method comprises assaying nucleic acid of a human or subject to determine a presence or an absence of a mutation altering the sequence or expression of vascular endothelial growth factor receptor-3 (VEGFR-3)/fme-like tyrosine kinase 4 (Filt4) allele (see AAG68952 and AB3764) and determining an increased risk of developing lymphatic disorder from presence or absence of the mutation. The presence of a mutation altering the encoded amino acid sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid correlates with an increased risk of developing a lymphatic disorder. Treatment for hereditary lymphatic disorder. Treatment for hereditary lymphatic disorder. Treatment for hereditary lymphatic acid correlates with an increased risk of developing a Lymphatic disorder. Treatment for hereditary sendothelial growth factor C (VEGF-C) and vascular endothelial growth factor C (VEGF-C) and vascular endothelial growth factor C (VEGF-C) and vascular endothelial growth factor C WEGF-C sequence is the coding sequence for VEGF-C
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                                                                                                                                                                                                          Human, gene therapy, lymphatic disorder, hereditary lymphedoema, Flt4, vascular endothalial growth factor receptor-3, VEGFR-3, VEGF-C, VEGF-D, fms-like tyrosine kinase 4; ss.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/packfiles1.seg:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-671-573B-32

US-08-671-573B-32

US-08-699-811-3

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APPLICANT: HU JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 0;
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961 GIGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGGCCAACCGAGAATTTGATGAAA 1020
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                      GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG 480
                                               421 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
                                                                                                                                       481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
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TELEFONMUNICATION INFORMATION:
TELEFONMER: (202)371-2500
TELEFONMER: (202)371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1674 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US B ASSIGNED FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
APPLICATION DATA:
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Best Local Similarity 100.0
Matches 1674; Conservative
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
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LOCATION: 12..80
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LOCATION:
FEATURE:
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, LOCATION:
US-09-042-105-1
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900 960 960 1501 TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC 1560

421 GTATAGATGTGGGGAAGGATTTGGAGTCGGGACAACACCTCTTTAAACCTCCATGTG 480 481 GTATAGATGTGGGGAAGGAGTTTGGAGTTGCGAACAACACTTCTTTAAACCTCCATGTG 480 481 TGTCGGTCTACAAATGTGGGGGTTGCCAATAGTGAGGGGCTGCAGTGAACACCA 540 481 TGTCGGTCTACAAATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 540 541 GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGGGCCTCTCTCT	Hardengerichteraangebechgegegebrichacecetharien gegebriche gebruich gegebrach gegebrac
5 B 5 B 5 B 5 B 5 B 5 B 5 B 5 B 5 B 5	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
ACACAATTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Thy Match 1. Thy Match 1. Local Similarity 100.0%; Score 10/4; DB 4; D

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Db 541 AGGAGCAGTTACGGTCTGTGTACAATGAACTCATGACTGTACTCTACCCAGAAT 600 241 ATTGGAAAATGTACAAGTCAAGGAAAGGAGCTGGCAACATAACAGAGACAGG 300 601 ATTGGAAAATGTACAAGTCAAGGAAAGGAGCTGGCAACATAACAGAGAACAGG 660 Oy 301 CCAACCTCAACTCAAGGACAGAAGAGACTTATAAATACAG 300 661 CCAACCTCAACTCAAGGACAGAAGACTTATAAATTTGCTGCAGCACATTATAATACAG 720 Oy 361 AGATCTTGAAAAGTATTGATAATGAGAGAAAAATTTGCTGCAGCACATTATAATACAG 720 Oy 421 GTATAGATGTGGAGAAGAGACAAAAACTCTTTAAACCTCCATGTG 480 OY 421 GTATAGATGTGGAGAGAGAGTTGGAGAAGACCAAACACCTCTTTAAACCTCCATGTG 480 OY 421 GTATAGATGTGGAGAGTTTGGAATTGGAGAACACCACTTTTAAACCTCCATGTG 480 OY 481 TGTCCGTCTACAGAAGGAGTTTGCAATAGTGAGGGGCTGCAATGTGAGACACCA OY 481 TGTCCGTCTACAGAAGAGATTTGAAATTACATGCAGGGCTGCAATGTGAACACCCA OY 691 GCACGAGCTACAGAAGAGTTTGAAATTACAGTGCATGCAT		DECEMBRICATION DECEMBRICA DECEMBRICA
	RESULT 5 US-09-313-299-1 Sequence 1. Application US/09313299B Sequence 1. Application US/09313299B GENERAL INFORMATION: APPLICANT: Lee, James APPLICANT: Lee, James APPLICANT: Lee, James APPLICANT: Wood, William I. TITLE OF INVENTION: VEGF-RELATED PROTEIN FILE REFERENCE: P06381D1 CURRENT APPLICATION NUMBER: US/09/313,299B CURRENT FILING DATE: 1999-05-17 EARLIER APPLICATION NUMBER: US 08/706,054 EARLIER APPLICATION NUMBER: US 60/003,491 BARLIER FILING DATE: 1995-08-08 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 1 LENGTH: 2031 TYPE: DNA	S S S S S S S S S S S S S S S S S S S

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1611 TGCTGCTCCCCGGGTCCTCGCGAGGCGCCCGCCGCCGCCGCCGCCTTCGAGTCCGGACTCG 1552
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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Wood, William I.
TITLE OF INVENTION: VEGF-Related Protein
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,054A
FILING DATE: 30-Aug-1996
CLASSIFICATION: <UNKNOWN>
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CORRESSPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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FILING DATE: 08-Sep-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08706054A Patent No. 6451764 GENERAL INFORMATION:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity
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                                                                              591 AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTAAAAAGGAAAGAAGTTCC
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US-09-313-299-2
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APPLICANT: Wood, William I.
TITLE OF INVENTION: VEGF-RELATED PROTEIN
FILE REPRENCE: P0963R1D1
CURRENT APPLICATION NUMBER: US/09/313,299B
CURRENT APPLICATION NUMBER: US/09/313,299B
CURRENT APPLICATION NUMBER: US/09/313,299B
EARLIER PRILING DATE: 1996-08-30
EARLIER APPLICATION NUMBER: US 60/003,491
EARLIER APPLICATION NUMBER: US 60/003,491
EARLIER PILING DATE: 1995-09-08
NUMBER OF SEQ ID NOS: 12
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Patent No. 6576608
GENERAL INFORMATION:
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Pred. No. 0;
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                         TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INPORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1674 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                         99.2%;
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Matches 1666, Conserv
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PCT-US96-09001-1
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TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 10
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CITY: ROSELAND
STATE: NOW JERSEY
COUNTRY: USA
ZIE: 07068
COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09001
FILING DATE:
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-288
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,968
FILING DATE: 6 JUN 95.
APPLICATION NUMBER: 08/207,550
FILING DATE: 8 MAR 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US96-09001-1; Sequence 1, Application PC/TUS9609001; GENERAL INFORMATION:
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                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION DATE:
PRIOR APPLICATION NUMBER: PCT/F196/00427
APPLICATION NUMBER: PCT/F196/00427
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATE: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATE: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 12-JAN-1996
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Pred. No. 0;
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ER: 28967/33691
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PRIOR APPLICATION DATA: 08/510,133
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERRORY/OCKET NUMBER: 28967/337
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 99.9%;
Matches 1653; Conservative C
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nucleic acid
SDNESS: single
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SEQUENCE CHARACTERISTICS:
LENGTH: 1997 base pair
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       COMPUTER READABLE FORM:
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STRANDEDNESS:
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US-08-795-430-7
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APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladdmir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
NUMBER OF SEQUENCES: 57
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGGCCAACCGAGAATTTGATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                    1021 ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
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                                                                                                         CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAGAACTAGACAGAAACTCATGCCAGT
                                                                                                                                                      901 CGGGGCTTCGGCCTGCCAGCTGTGTGTGTGTGTGTAGAACTAGAAACTAGAAACTCATGCCAGT
                                                                                                                                                                                                                                                                                               961 GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGRGGGGCCAACCGACAATTTGATGAA
                                                                                                                                                                                                                                                                                                                                                                     ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u> AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGATGCTCC</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08795430 Patent No. 6130071 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-795-430-7
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                                                                        NAME: Gass, David A.

REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELERX: 312/474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1997 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNISS: single
                                                                                                                                                                                                                                                                                                                            Query Match

98.7%; Score 1651.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1653; Conservative 0; Mismatches
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-11995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    ) NAME/KEY: CDS

: LOCATION: 352.1608

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-355-700-7
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GENERAL INFORMATION:

APPLICANT: Alitalo, Kari
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marefall, O'Toole, Geretein, Murray & Borun
STREET: Glad Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Ilinois
COUNTRY: United States of America
ZIP: G606-640.
ZIP: G606-640.
MEDIWA TYPE: PROPRY disk
COMPUTER READALE FORM:
MEDIWA TYPE: PREMIT Relase #1.0, Version #1.25
CONFOTTER: PREMIT RELEASE
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LOCATION:
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US-08-601-132-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6.300 Sears Tower, 233 South Wacker Drive CITY: Chicago CITY: Chicago COUTRY: United States of America COUNTRY: United States of America CONPUTER ELADABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: ABLOCHIN PC.DOS/MS-DOS SOFTWARE: PARCHING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PARCHING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PARCHING NUMBER: 18-08/601,132 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133 PRIOR APPLICATION NUMBER: 08/510,133 PRILING DATE: 12-JAN-1996 PRIOR APPLICATION NUMBER: 08/510,133 PRILING DATE: 10-MG-1995 ATTORNEY/AGENT INPORMATION:
NAME: GASE, DAVIG A 38,153 REPERBRICE/DOCKET NUMBER: 28967/33348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                             GCAAAATATGTTTAAAATAAAATGAAAATTGTATT 1655
                                                                                                                                                                                                                                                                                    GCAAAATATGTTTAAAATAAAATGAAATTGTATT 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.7%; Score 1651.8;
llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                               RESULT 13

US-08-671-573B-32

US-08-671-573B-32

Sequence 32, Application US/08671573B

Patent No. 6645933

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Alitalo, Cari

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28
TELECOMONINICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1997 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 1653; Conserv
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, LOCATION:
US-08-671-573B-32
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Best Local Similarity
Matches 1526; Conserv
                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
; LOCATION:
US-08-999-811-3
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1081 AATGTGCCTGTGAAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAAGGAAGTTCC 1140
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                              AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGTTCC
                                                               ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACGGCCAGAAGGCTTGTGAGC
                                                                                          1481 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGG
                                                                                                                                                                                            AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTTCTATTATGGAAAACTGTGT
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APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDEADER: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STREET: 1100 NEW YORK AVENUE
COUNTRY: USA
ZATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN PC-DOS/NS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/207,550
FILING DATE: 08-MAR-1994
PRIOR APPLICATION NUMBER: US 08/207,550
FILING DATE: 06-JUN-1995
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Patent No. 5932540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 TATAAAATTTGCTGCAGCACATTATAAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGACAAACACCTTTTAAACCTCCATGTGTCCGTCTACAGATGTGGGGGTTGCTG
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NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REGISTRATION NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2500
TELEPHONE: (202)371-250
TELEPHONE: (202)371-250
TELEPHONE: (202)371-250
TELEPHONE: (202)371-250
TELEPHONE: (202)371-250
TENGTH: 1526 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
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                                                                                                                             ZIF: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREWITH
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMARR:
GLASSIFICATION:
FILING DATE:
APPLICATION NUMBER: US 08/207,5S0
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 24-DEC-1997
CLASSIFICATION:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: Z4-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.10000C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMA
STREET: 1100 NEW YORK AVENUE CITY: WASHINGTON
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91.2%; Sco
Best Local Similarity 100.0%; P:
Matches 1526; Conservative 0;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1526 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
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143..1120
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71..1120
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NAME/KEY:
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LOCATION:
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US-09-042-105-3
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       GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
                                                                661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
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Patent No. 6040157
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CRO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTATTTATAAAAAAAAAAAAA 1526
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US-09-042-105-3
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P S		301	CGCGACAAACACCTTCTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG 508 	දු පු		1529 TV
y d		509	CAATAGTGAGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT 5	S G		1589 AV
1 & A		569	TGAAATTACAGTGCCTCTCTCTAGGCCCCAAACATAACATCAGTTTTGCCATCA TGAAATTACAGTGCCTCTCTCTCAGGCCCCAAACAGATCAGTTTTGCCAATCA	S S		1649 T. 1501 T.
oy Bb		629	CACTICCIGCCGAIGCAIGTCIAAACIGGAIGTITACAGACAAGIICATICCATIATIAG 688 	Se	Search completed Job time : 152 8	pletec 152 g
<i>∂</i> 8		689	ACGITCCCTGCCAGCAACACTACCACAGAGCAGCGAACAAGACCTGCCCCACCAA 748 			
S an		749	TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTTATGTTTTCCTC 808			
g &		809	GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAACAAGGGCT 868 			
95 PP		869	GGATGAAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTTCGGCCTGCCAGCTGTGGACC 928 			
g S		929	CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAAC			
\ \ \ \ \		989	CCAATGTGGGGCCAACCGAGAATTTGATGAAACACATGCCAGTGTGTATGTA			
S A		1049	CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC 1108: 			
8 8		1109	ACAGAAATGCTTATAAAAGGAAAGAACTTCCACCACCAACATGCAGCTGTTACAGACG 1168 			
දු දු		1169	GCCATGTACGAAACGCCTGGTGAGCCAGATTTTCATATAGTGAAGAGTGTG 1228 			
중 음		1229	TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTFTTCCA 1288		-	
& g		1289	GTTCATCGAFTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGT			
8 S	ē	1349	GAGACCCTTGTGGGTCCATGCTAACAAGACAAAAGTCTGTCT			
95 25		1409	TAACTTTACAGAAATGGACTGGGGGCCTCTGGGAAGGCCTCTTGTAAAGACTGGTTTT 1468 			
දු දු	•	1469	CIGCCAAIGACCAAACAGCCAAGAITITCCTCTIGIGAITICTITAAAAGAATGACTAIA 1528 			•
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earch completed: February 25, 2004, 22:07:19 ob time : 152 secs

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100.0%; Score 1674;
11 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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US-09-935-726-1
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NAME/KEY: sig_peptide
LOCATION: (12)..(80)
NAME/KEY: CDS
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Matches 1674;
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278.2
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231.8
227
212.6
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Appl
                                                                                                                                                      February 25, 2004, 19:10:43; Search time 621 Seconds (without alignments) 9439.215 Million cell updates/sec
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Sequence 1, P
Sequence 1, P
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2: /cgn2_6/ptodata/1/pubpna/PCT_TBW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/PCT_TBW PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-921-143-1
US-10-120-398-1
US-10-120-398-1
US-10-120-398-1
US-10-120-377-1
US-10-346-802-1
US-10-346-802-2
US-09-795-0068-21
US-09-795-0068-21
US-09-375-248-3
US-09-375-248-3
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US-10-262-538-7
US-10-061-126-3
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence 1, Application WS/09935726;
Bublication No. US20030008357A1
GENERAL INFORMATION:
APPLICANT: Hu, Jin-Shan
APPLICANT: Crad, Liang
TITLE OF INVENTION: Vascular Endothelial Growth Factor-2;
FILE REFERENCE: PF112P3D1C1
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US/09/935,726
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1674
1. US 09-21-143-3

1. US 09-221-143-3

1. US 09-221-143-3

2. US 09-235-726-3

3. US 09-935-726-3

4. US 10-120-414-3

4. US 10-120-143-36

4. US 10-120-1386-12

5. US 10-121-143-36

6. US 10-121-143-36

7. US 10-121-143-36
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181	AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG TTTACAGACAACAACTACATTTTTATATACACTTCCTGCCGACACATGTCTAAACTGGATGT TTTACAGACAACATCATTTTATATATACATTTTTATATACATGTGGAATAATCACATTCCACAGTGCC AGGCAGCGAACAACATTCATTTATATATACATTTTGGAATAATCACATTCCACAGTGCC AGGCAGCGAACAACATTATATATATACATTTTTCCTCCGAATTGCCAAACAACAACAACAACAACACACCACCACTCCCAATTACATTTATATATATACATTTTCCTCC

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; Sequence 1, Application US/10120398
; Publication No. US20030170786A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2; FILE REFERENCE: PF112P7
; CURRENT APPLICATION WUMBER: US/10/120,398
; CURRENT FILING DATE: 2002-04-12
; PRIOR PILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.1
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SEQ ID NO 1
LENGTH: 1674
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100.0%; Score 1674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1674; Conservative 0; Mismatches
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                                                                                                               NAME/KEY: CDS
LOCATION: 12..1268
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                              mat peptide
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US-10-140-1
; Sequence 1, Application US/10120414
; Sequence 1, Application US/10120414
; Publication No. US20030175274A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, Craig, et al.
; TITLE OF INVENION: Vascular Endothelial Growth Factor-2; FILE REFRENCE: PF112P9
; CURRENT APPLICATION NUMBER: US/10/120,414
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION: NUMBER: 60/283,385
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2001-04-13
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Best Local Similarity 100.0%;
Matches 1674; Conservative 0
               FEATURE:

NAME/KRY: eig peptide

LOCATION: (12)..(80)

OTHER INFORMATION:

FEATURE:

NAME/KRY: CDS

LOCATION: (12)..(1268)

OTHER INFORMATION:

FEATURE:

NAME/KEY: mat_peptide

LOCATION: (81)..()

COTHER INFORMATION:

UCCATION: (81)..()

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   Homo sapiens
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TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REFERENCE: PF112P8
CURRENT APPLICATION NUMBER: US/10/120,377
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Publication No. US20030176674A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig, et al.
TILE OF INVENTION: Vascular Endotl
FILE REFERENCE: PF112P8
CURRENT APPLICATION NUMBER: US/10//
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (12)...(80)
OTHER INFORMATION:
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NAME/KEY: mat_peptide

LOCATION: (81)...()

OTHER INFORMATION:
US-10-120-414-1
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LOCATION: (12)..(1268)
OTHER INFORMATION:
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US-10-346-802-1
Sequence 1, Application US/10346802
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CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/283,391
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/317,600
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN Version 3.1
LENGTH: 1674
TYPE: DNA
ORGANISM: HOMO Sapiens
FEATURE:
NAME/KEY: Sig_Peptide
LOCATION: (12)...(80)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (12)...(1268)
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OTHER INFORMATION:
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Matches 1674; Conserv
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                      APPLICANT: Lee, James
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: VEGF-RELATED PROTEIN
FILE REFERENCE: POSGSRIDI
CURRENT APPLICATION NUMBER: US/10/346,802
CURRENT FILING DATE: 2003-01-17
PRIOR PELICATION NUMBER: US/09/313,299B
PRIOR FILING DATE: 1999-05-17
PRIOR PELING DATE: BARLIER APPLICATION NUMBER: US 60/0
PRIOR FILING DATE: BARLIER FILING DATE: 1996-08-30
PRIOR FILING DATE: BARLIER FILING DATE: 1995-09-08
NUMBER OF SEQ ID NOS: 12
LENGTH: 2031
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Pred. No. 0;
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Best Local Similarity 99.8%;
Matches 1667; Conservative
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; LOCATION: 1-2031
; OTHER INFORMATION:
US-10-346-802-1
     GENERAL INFORMATION:
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%Sequence 2, Application US/10346802
%Bublication No. US20030166873A1
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Lee, James
TITLE OF INVENTION: VEGE-RELATED PROTEIN
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CTHER INFORMATION: Incyte ID No. US20030119009A1 550425CB1

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                                                                  ACTIVATION
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APPLICANT: Susan Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon M. Shoh
TITLE OF INVENTION: GENES REGULATED BY MYCN ACT
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT APPLICATION NUMBER: 00/270.
CURRENT APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGram
SQCTWARE: PERL PROGram
SEQ ID NO 98
LENGTH: 1786
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.7
Matches 1667; Conservative
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Patent No. US20020151680A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR;
TITLE OF INVENTION: BUNDOTHELIAL GROWTH FACTOR DNA9 AND PROTEINS
FILE REFERENCE: 28967/35977B
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CURRENT FILING DATE: 2003-01-17
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FRIOR APPLICATION NUMBER: US/99/313,299B
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/97/97 FILING DATE: 1999-05-17
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/97/97 FILING DATE: 1996-08-30
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/97/97 FILING DATE: 1996-09-08
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
LENGTH: 2031
TYPE: DNA
CREATURE:
NAME/KEY: Human
FEATURE:
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/ OTHER INFORMATION: Sequence source:
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Publication No. US2003002675941
GENERAL INFORMATION:
APPLICANT: Ferrell, Robert E.
APPLICANT: Finegold, David N.
APPLICANT: Finegold, David N.
APPLICANT: Finegold, David N.
APPLICANT: Earkainen, Marika
TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
TITLE OF INVENTION: THE FERING AND FILE REFERENCE: 28967/35255A
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CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT FILING DATE: 2001-02-26
FRIOR APPLICATION NUMBER: US 60/205,331
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/185,205
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: 1997
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                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.9'
Matches 1653; Conservative
                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (352)..(1608)
US-09-795-006A-21
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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US-10-201-386-7
Sequence 7, Application US/10201386
Publication No. US20030091567A1
GENERAL INFORMATION:
GENERAL INFORMATION, Kari
TILLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C)
TITLE OF INVENTION: AND GENE, MUTANITS THEREOF, AND USES THEREOF
FILE REFERENCE: 25967/34140A
CURRENT APPLICATION NUMBER: US/10/201,386
GURRENT FILING DATE: 2002-07-23
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CURRENT APPLICATION NUMBER: US/09/375,248
CURRENT FILING DATE: 1999-08-16
EARLIER APPLICATION NUMBER: PCT/US99/06133
EARLIER FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIN Ver. 2.0
LYPE: DATA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (352)...(1611)
FRATURE:
COTHER INFORMATION: Human CDNA for prepro-VEGF-C
US-09-375-248-3
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98.7%; Score 1651.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1653; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US/09/534,376
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1090-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR PLING DATE: 1999-11-05
PRIOR PLING DATE: 1996-02-02
PRIOR PLING DATE: 1996-02-02
PRIOR PLING DATE: 1997-02-05
PRIOR PRIOR PRIORICATION NUMBER: 08/795,430
PRIOR FILING DATE: 1996-06-1
PRIOR PRIOR DATE: 1996-01-1
PRIOR PLING DATE: 1996-01-1
PRIOR FILING DATE: 1996-01-1
PRIOR FILING DATE: 1996-02-14
PRIOR FILING DATE: 1996-02-14
PRIOR FILING DATE: 1996-01-12
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PRIOR PLING DATE: 1996-01-12
PRIOR FILING DATE: 1996-01-12
PRIOR FILING DATE: 1996-01-13
PRIOR FILING DATE: 1996-01-14
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 7
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NAME/KEY: CDS
LOCATION: (352)..(1608)
COTHER INFORMATION: prepro VEGF-C CDNA
US-10-201-386-7
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TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
FILLE REPERENCE: 28967/37564
CURRENT APPLICATION NUMBER: US/10/262,538
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 1997
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Publication No. US20030113324A1
GENERAL INFORMATION:
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APPLICANT: De Vries, Gerald W.
TITLE OF INVENTION: Methods of Extending Corneal Graft
TITLE OF INVENTION: Survival
FILE REFERENCE: P-AR 4951
CURRENT APPLICATION NUMBER: US/10/081,126
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                              DB 14;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                            98.7%;
larity 99.9%;
Conservative (
                                                                                                                                                                                                                         NAME/KEY: CDS
; LOCATION: (372)...(1628)
US-10-081-126-3
                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Simi
Matches 1653;
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                                                                                                                                                        LENGTH:
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Perfect score:

Sequence:

OM nucleic -

Run on:

Scoring table:

Searched:

Database :

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CA421508 UI-H-FG0-AW195617 xn844911.x
AA923193 om48d611.s
AA923193 om48d611.s
AA923193 om48d611.s
BUG10991 UI-H-FD1-BE218812 hv45a10.x
BUG005831 UI-H-FD1-BE218812 hv45a10.x
BE218812 hv45a10.x
BE218812 hv45a10.x
BE218812 hv45a10.x
BM12718 ie95f08.x
AM151613 z127h03.s
BM054973 ie95f08.x
AM341345 xz38f10.x
BE6705473 602120178
BE6705473 602120178
BE6705473 602120178
BE57050 vf34f01.x
BE57050 vf34f01.x
BE58208 601644672
BM113454 BX113454
BE58208 601644672
BM15807 ty96h12.x
AA455340 ty96h12.x
AA455340 ty96h12.x
AA459340 ty96h12.x
AA459340 ty96h12.x
BM15803 UI-H-BI2-BM11008
AW37803 UI-H-BI1-BE22114 hu06a11.x
BM31780 yy15d12.s1
BM317803 UI-H-BI1-BE3765 AGENCOURT
BE376968 601227146
AA406492 zv12g06.t
AN06442 zv12g06.t
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2450 bp mRNA linear HTC 20-SEP-2003
Mus musculus 16 days embryo head cDNA, RIKBN full-length enriched
library, clone:Cl30004M09 product:vascular endothelial growth
factor C, full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
                                                                AA923193
AW070215
BW070215
BW107199911
BW0199911
BW107196
BW107186
AA151613
BW054972
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AK047844.1 GI:26339001
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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465.6
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        AK047844 Mus muscu
BG677890 602625584
BG680919 602628716
CA488579 AGENCOURT
                                                                                                                                             February 25, 2004, 16:56:30; Search time 3995 Seconds (without alignments) 12512.964 Million cell updates/sec
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                                                                                                                                                                                                                                                                         Description
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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50.1
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1207.6 839.4 782.4 780.8

Score

Result No.

9

Gaps

19;

283

343

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511 420 571

JOURNAL

TITLE

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GGEVKAPEGKDLBEQLRSVSSVDELMSVLYPDYWKMYKCQLRKGGWQDPTLNTRTGDS VKRAAAHYNTBEIKSPENSWYRCGG CKRAAAHYNTBEIKSPENSWYRCGG CKRAAAHYNTBEIKSPENSWAKTCQDRRBEWCIDWGKBFGAAHYNTBEIKSPENSKRCGG CKNSELJCCMNTSTTYNETRIFSCTYBERCHTSPENSTGGGRENDTSTROGGENTSTROGGENTSTTYPLSCGGRENTISFAAHTSCRCMSKLDYRRCHG SITRRSLBATLPQCQAANKTCPTNYVMNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVC CQPNKELDBDDTQCVCKGGLRPSSCGFHKELDRDSCQCVCKNKLFPNSCGANRBFDENT CQCVCKRTCFRNQPLNFGKCACFLKGKKFHHQTCSCYRRPCANRLKHCD PGLSFSBEVCRCVPSYWKRPHIN"
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Best Local Similarity 85.6%;
Matches 1418; Conservative
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiwagi,K.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.,
RIKEN integrated sequence analysis (RISA) system--384-format
Genome Res. 10 (11), 1757-1771 (2000)
B. 1076861
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Sadchi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hirancto, K., Hirackar, T., Hirozane, T., Haysihda, K., Hayataw, T., Kono, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kaukawa, T., Koya, S., Kurihara, C., Mareuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numara, M., Sakazume, N., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Saqabe, Y., Taqami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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/db xref="GI:26339002"
/translation="MHLLCFLSLACSLLAAALIPSPREAPATVAAFESGLGFSEAEPD
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Submitted (16-UUI-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
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vascular endothelial growth factor C (MGD|MGI:109124,
GB|NM_009506, evidence: BLASTN, 99%, match=1784)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
I. 24go.in.gsc.riken.go.jp/
Acation/Qualifiers

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/ ptrain="C57BL/6"
/ db_xref="FANYOM DB:C130004M09"
/ db_xref="MG1:24]5670"
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| / organism="Homo sapiens" |
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| / clone=lib="NCI_CGAP_Skn4" |
| / clone=lib="NCI_CGAP_Skn4" |
| / note="Organ: 8kin; Vector: pcWV-SPORT6; Site_I: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0605 row g column: 22
High quality sequence stop: 806.
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 998)
CGGGGCTTCGGCCTGCCAGAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
                                               GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
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AGENCOURT 10808789 MAPCL Homo sapiens cDNA clone IMAGE:6720351 5', CA488579
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Marional Itosas 1 to 858

National Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
CCTTCGAGTCCGGACTCGGACCTCTCGGACGCGGACGCCGACGCGGGGCGACGCGGGCCTT
                                                                                             ATGCAAGCAAAGATCTGGAAGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAAGATCTAAAGA
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E 1 (bases 1 to 831)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Townord Colomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Library Preparation: Column: 04

High quality sequence stop: 810.
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602628716F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4753755 5',
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NOT CAPS Stn4"
/note="Organ: skin, Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: skin, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 2.5e-118;
); Mismatches 1; Indels 4;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4753755"
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Similarity 99.4%;
37; Conservative (
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, Dento-soares@aliowa.edu
The following repetitive elements were found in this CDNA
sequence: 1-53, APT rich#Low_complexity (matched compliment)
BOLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA421508
UI-H-FGG-bcu-e-12-0-UI.sl NCI CGAP ENI 2 Homo sapiens cDNA clone
UI-H-FGG-bcu-e-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                         721 CAGAAATGCTTGTTAAAAGGAAAGTTCCACCACAAACATGCAGCTGTTACAGAACG 780
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 750)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP),
Umpublished (1997)
                                                   TGCCCCAGAAATCAACCCCCTAAATCCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCA
                                                                                                         661 TGCCCCAGAAATCAACCCCTANATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCA
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CA421508.1 GI:24784163
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DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM14279 row: 1 column: 15
    High quality sequence stop: 674.
    Location/Qualifiers
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    location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GABATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630 ACTICCIGCCGAIGCATGICIAAACIGGAIGITIACAGACAAGIICAIICCAITAITAGA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAAT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GGTTCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACAAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTCG 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 Tacardradanaarcacardradangcardacheacheachadaarrrrandringcered 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAAGAAGGAGCTG 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GAIGCIGGAGAIGACICAACAGAIGGATICCAIGACAICTGIGGACCAAACAAGGAGCIG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAAGAGACCTGTCAGTGTCTGCAGAGCGGGCTTCGGCCTGCCAGCTGTGGACCC 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAAAGACTCAATGCATGCCACGGGGGGGGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 AGAAAGACTCAAIGCAIGCCACGGGAGGIGIGIAIAGAIGIGGGGAAGGAGIIIIGGAGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCGACAAACACCTTCTTTAAACCTCCATGTGTCTCCGTCTACAGATGTGGGGGGTTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 AATAGTGAGGGCTGCAGGATGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATAGTGAGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         570 GAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.6%; Score 780.8; DB 14 ilarity 99.0%; Pred. No. 4.6e-118; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 816; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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/mol type="mono" sapiens
/mol type="mono" sapiens
/do xref="taxon:9666"
/clone="UI-H=FH0-bco-p-03-0-UI"
/tissue type="HH0-bco-p-03-0-UI"
/tissue type="HH0-bco-p-03-0-UI"
/tissue type="HH0-bco-p-03-0-UI"
/do stage="Adult"
/lab_host="HH0B (Life Technologies)"
/clone="Cygan: Bone; Vector: pT7T3-Pec (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
/modified polylinker; Site 1: EcoR I; Site 2: Not I;
/modified polylinker; Site 1: EcoR I; Site 2: Not I;
/modified polylinker; Site 1: EcoR I; Site 2: Not I;
/modified polylinker; Site 1: EcoR I; Site 2: Not I;
/modified polylinker; Site 1: EcoR I; Site 2: Not I;
/modified polylinker; Site 1: EcoR I; Site 3: Not I;
/modified polylinker; Site 1: EcoR I; Site 3: Not I;
/modified polylinker; Site 1: EcoR I; Site 3: Not I;
/modified polylinker; Site 3: Not I; and cloned containing Not I adaptor, dispersed with an oligo-dT primer containing Not I site purples of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AdAMTCGGC. The cell line was provided by Dr James Martin from University of Iowa

TAG TISSUE-Human Chondrosarcoma Cell Line CSB - Grade 1
                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-51, AT_rich#Low_complexity (matched compliment)
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 GTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCTGTTACA
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.larity 99.2%; Pred. No. 1.1e-109;
Conservative 0; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .748
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Matches 743; Conserv
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       JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                           1045 GAACCTGCCCCAGAAATCAACCCCTAAAATCCTGGAAAATGTGCCTGTGAATGTACAAGAAA
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       DB 14; Length 750;
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   Score 730.6; DB 14;
Pred. No. 7.8e-110;
0; Mismatches 5;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the limits clone state available royalty-free through LLNL; contact the limits clone state available royalty-free through LLNL; contact the limits clone giber stop: 498.

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Amol filed polylinker; Site 1: Not 1; Site 2: Eco R1;

Equal amounts of plasmid DNA from three normalized

Ilbraries (fetal lung NBHL19W, testis NHT, and B-cell

NCI CGAP GCB1) were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                           TITICIGCCAATGACCAAACAGCCAAGATTTTCCTTGTGATTTCTTTAAAAGAATGAC 1524
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    Length 808
                                             Indels
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  Score 702; DB 10;
Pred. No. 3.7e-105;
0; Mismatches 41;
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Matches 760; Conservative
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    234 TGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAAGAC 175
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 728)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2601 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
                                                                                                                                             114 ATATIGITICIGCATICATITITATAGCAACAACAATIGGTAAAACTCACTGIGATCAAT
                                                                                                                                                                                                      174 CAAGATTTTCCTCTTGTGATTTCTTTAAAGAATGACTATATAAATTTTTCCACTAAAA
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728 bp mRNA linear EST 20
8x809010.x1 Scares NFL T GBC_S1 Homo sapiens CDNA clone
IMAGE:2567826 3' Similar to SW:VEGC HUMAN P49767 VASCULAR
ENDOTHELIAL GROWTH FACTOR C PRECURSOR ', mRNA sequence.
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Pred. No. 1.9e-99;
0; Mismatches 14;
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llarity 97.7%;
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                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (infodimage.llnl.gov) for further information.
Insert Length: 785
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 476.

Location/Qualifiers
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sequence: 1-53, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
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99.5%; Pred. No. 1.2e-97; Mismatches 3; Indels
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TAG_LIB=UI-H-EDO
TAG_SEQ=CGTCAAGGCT"
                                                                      Location/Qualifiers
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UI-H-ED0-ayr-n-11-0-UI.S1 NCI_CGAP_ED0 Homo sapiens cDNA clone
IMAGE:5842762 3', mRNA sequence.
                                                                                                                               GAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAAAATGCAGCTGTTACAGACGGCC 1171
                                                                                                                                                                                                          ATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTCG 1231
                                                                                                                                                                                                                                                                                         TIGIGICCCTICATATIGGCAAAGACCACAAATGAGCTAAGAITGTACTGTTTTCCAGTT 1291
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Email: cgapbs-r@mail.nih.gov

Itsue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov

The following repetitive elements were found in this cDNA
          GGTGGGGCAACCCGAGATTTGNATGAAAACACATGCCAGNTGTGTATGTAAAGAACCTG 610
                                                                                                                                                                                                                                                    430
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                                                                        CCCCAGABATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCCACA
                                                                                                                                                       GAAATGCTTGTTAAAAAGGAAAGAAGTTCCACCACCAAACATGCTGTTACAGACGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 ATTTATTTCCACTAAAATATTGTTTCTGCATTCATTTTATAGCAACAACAATTGGTAA
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Pred. No. 1.8e-96; 0; Mismatches 5;

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1074 CCTGGAAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAG 1133
                                                                                                       GATGAAAACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAAT
                                                                                                                                                                                    597 CCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAG
                                                                1014 GATGAAAACACGAGTGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAAT
                         652; Conservative
      Best Local Similarity
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//done lib NOI Cape Fil is a normalized cDNA library
derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pr773-Per vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GAGGTCGGTC. The cell lines were provided by Dr. James
Martin from the University of lowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-48, AT_rich#Low_complexity (matched compliment)
POLYA=Yes.
                                                                                                                                                                                                                                                                                BUG19991 657 bp mRNA linear EST 23-SEP-2002 UI-H-FLI-bfv-p-05-0-UI:81 NCI_CGAP_FLI Homo sapiens cDNA clone UI-H-FLI-bfv-p-05-0-UI 3', mRNA sequence.
                                                            TITCIGCATICATITITATAGCAACAACAATIGGIAAAACICACIGIGAICAAIATITIT 63
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                            SSUE=Human Chondrosarcoma Grade 3 cell line mix
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/db_xref="taxon:9606"
/clone="UI-H-FL1-bfr-p-05-0-UI"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
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Length 657;

DB 13;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 AAGTITCCACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCT
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1134 AAGTTCCACCACCAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCT
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/tissue type="carcinoid"
/lab_host="bH108"
/clone_lib="NoI_CGAP_Lu24"
/lone_lib="NoI_CGAP_Lu24"
/note="forgan: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 14,4920-14,17991 and 1520904-1522439). Subtraction by Bento Soares and M. Patima Bonaldo.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@inage.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 449.
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1...622
| organism="kmono sapiens" |
| wol type="mRNA" |
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CB854820 622 bp mRNA linear EST 22-APR-2003 UI-CF-EC1-ack-o-03-0-UI.sl UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-ack-o-03-0-UI 3', mRNA sequence.
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Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Lekaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 622)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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The following repetitive elements were found in this cDNA sequence: 1-53, AT rich#Low_complexity (matched compliment) Seq primer: M13 FORWARD POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Iowa
2013 University of Iowa Med Labs, Iowa City, IA 52242, USA
1213 1319 366 171
Fax: 319 356 7171
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Pred. No. 7.9e-91;
0; Mismatches 4; I
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TAG_SEQ=None found"
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al Similarity 99.4%;
617; Conservative
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AATGCTTGTTAAAAGGAAAGTTCCACCACCAAACATGCAGCTGTTACAGACGGCCAT 1173
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/mol type="mRNA"
/db xref="taxon:10090"
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/tissue_type="undifferentiated limb" | /tissue_type="undifferentiated limb" | /tib host="DRIOB (Dage-resistant)" | /clone lib="NHH MGC 134" | /note="Vector: pcMV-SPORT6.1; Site 1: EcoRV; Site_2: NotI; Cloned undidrectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NHH_MGC Library."
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Pred. No. 5.7e-89;
0; Mismatches 115;
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/close libe.Melton Normalized Human Islet 4 N4-HIS 1."
/note="Organ: Pancreas; Vector: pSPORTI; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size selected by column
fractionation, average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
library. "Application of the stranded contromatography and used to make this
                                                                                                                                                                                                                                                                                                           Entraryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

Ammalia, Eutheria; Primates; Catarrhini, Hominidae, Homo.

1 (bases I too S84)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl; G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theislain, B., Kniter, E., Ronko, I., Bennett, J., Varken, Y., Milliams, T., Jackson, Y. and Bowers, Y. Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTS: 1e95f08, yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                       BM127186

584 bp mRNA linear BST 12-MAR-2002
195508.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5674886 3' similar to SW:VBGC HUMAN P49767
VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 617-495-857

Fax: 617-495-857

Email: dmeltonobiohp, harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Juliana Brown

(brown@fass.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov

seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .584
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: -400r 110m 5100; 448.
High quality sequence stop: 448.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5674886"
                                                                                                                                                                                                     BM127186.1 GI:17121738
                                                                                                                                                                                                                                                            Homo sapiens (human)
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584 TGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCAC 525
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February 25, 2004, 22:04:40 completed:

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Gaps

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Score 576; DB 12; Length 584; Pred. No. 1.7e-84; 0; Mismatches 5; Indels (

Query Match Best Local Similarity 99.1%; Matches 579; Conservative